GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 28, 2003, 15:13:35 ; Search time 1515 Seconds
(without alignments)
270.031 Million cell updates/sec

Title: US-09-335-032-71
Perfect score: 10
Sequence: 1 cttctctttt 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		10	100.0	10	6	BD065135	BD065135 Character
2	c	10	100.0	12	6	AR029992	AR029992 Sequence
3		10	100.0	12	6	AR030057	AR030057 Sequence
4	c	10	100.0	17	6	AX500413	AX500413 Sequence
5	c	10	100.0	17	6	AX500414	AX500414 Sequence
6	c	10	100.0	17	6	AX500415	AX500415 Sequence
7	c	10	100.0	17	6	AX500416	AX500416 Sequence
8	c	10	100.0	17	6	AX500417	AX500417 Sequence
9	c	10	100.0	17	6	AX500418	AX500418 Sequence
10	c	10	100.0	17	6	AX500419	AX500419 Sequence
11	c	10	100.0	17	6	AX500420	AX500420 Sequence
12		10	100.0	17	6	AX673153	AX673153 Sequence
13		10	100.0	19	6	AX659410	AX659410 Sequence
14	c	10	100.0	20	6	AR315845	AR315845 Sequence
15		10	100.0	20	6	I48976	I48976 Sequence 3
16	c	10	100.0	21	6	AR054595	AR054595 Sequence
17	c	10	100.0	21	6	AR136775	AR136775 Sequence
18	c	10	100.0	21	6	E35992	E35992 Method for
19		10	100.0	22	6	AR029876	AR029876 Sequence
20		10	100.0	22	6	AX352316	AX352316 Sequence
21		10	100.0	22	6	AX352317	AX352317 Sequence
22		10	100.0	22	6	AX352318	AX352318 Sequence
23	c	10	100.0	24	6	AR069183	AR069183 Sequence
24	c	10	100.0	24	6	AR102693	AR102693 Sequence
25	c	10	100.0	24	6	AR175558	AR175558 Sequence
26	c	10	100.0	24	6	AX443310	AX443310 Sequence
27	c	10	100.0	24	6	BD090389	BD090389 A method
28	c	10	100.0	24	6	BD176467	BD176467 A method
29	c	10	100.0	24	6	I64401	I64401 Sequence 17
30	c	10	100.0	25	6	AX502410	AX502410 Sequence
31	c	10	100.0	25	6	AX502411	AX502411 Sequence
32	c	10	100.0	25	6	AX502412	AX502412 Sequence
33	c	10	100.0	25	6	AX502413	AX502413 Sequence
34	c	10	100.0	25	6	AX502414	AX502414 Sequence
35	c	10	100.0	25	6	AX502415	AX502415 Sequence
36	c	10	100.0	25	6	AX502416	AX502416 Sequence
37	c	10	100.0	25	6	AX502417	AX502417 Sequence
38	c	10	100.0	25	6	AX502418	AX502418 Sequence
39	c	10	100.0	25	6	AX502419	AX502419 Sequence
40	c	10	100.0	25	6	AX502420	AX502420 Sequence
41	c	10	100.0	25	6	AX502421	AX502421 Sequence
42	c	10	100.0	25	6	AX502422	AX502422 Sequence
43	c	10	100.0	25	6	AX502423	AX502423 Sequence
44	c	10	100.0	25	6	AX502424	AX502424 Sequence
45	c	10	100.0	25	6	AX502425	AX502425 Sequence
46		10	100.0	25	6	I48977	I48977 Sequence 4
47	c	10	100.0	26	8	ATH525492	AJ525492 Arabidops
48	c	10	100.0	26	8	ATH525503	AJ525503 Arabidops
49	c	10	100.0	27	6	AR066258	AR066258 Sequence
50	c	10	100.0	27	6	AR191561	AR191561 Sequence
51	c	10	100.0	27	6	AX115839	AX115839 Sequence
52		10	100.0	28	6	AX040823	AX040823 Sequence
53		10	100.0	29	6	AR261655	AR261655 Sequence
54		10	100.0	30	6	AR261654	AR261654 Sequence
55		10	100.0	30	6	AR261656	AR261656 Sequence
56		10	100.0	30	6	AR261657	AR261657 Sequence
57	c	10	100.0	33	6	AR120483	AR120483 Sequence
58	c	10	100.0	33	6	BD063492	BD063492 Streptoco
59		10	100.0	33	6	E36416	E36416 dna G. 6/20
60	c	10	100.0	38	6	AX218433	AX218433 Sequence
61		10	100.0	38	6	AX220343	AX220343 Sequence
62	c	10	100.0	38	6	AX273375	AX273375 Sequence
63		10	100.0	40	6	BD182426	BD182426 Human art
64		10	100.0	42	6	I12092	I12092 Sequence 33
65		10	100.0	43	6	AX484623	AX484623 Sequence

c	66	10	100.0	45	6	AX061875 AX061875 Sequence
c	67	10	100.0	45	8	ATH528602 AJ528602 Arabidops
	68	10	100.0	47	6	AR284713 AR284713 Sequence
c	69	10	100.0	47	6	AR288787 AR288787 Sequence
	70	10	100.0	47	6	AR289547 AR289547 Sequence
	71	10	100.0	47	6	AR289811 AR289811 Sequence
c	72	10	100.0	47	6	AR290737 AR290737 Sequence
c	73	10	100.0	47	6	AR291549 AR291549 Sequence
c	74	10	100.0	50	6	AR139658 AR139658 Sequence
	75	10	100.0	50	6	AX158156 AX158156 Sequence
	76	10	100.0	51	6	AX118141 AX118141 Sequence
	77	10	100.0	51	6	AX158155 AX158155 Sequence
	78	10	100.0	51	6	AX160381 AX160381 Sequence
	79	10	100.0	51	6	AX160382 AX160382 Sequence
	80	10	100.0	51	6	AX160383 AX160383 Sequence
	81	10	100.0	51	6	AX165562 Sequence
	82	10	100.0	51	8	ATH521150 AJ521150 Arabidops
c	83	10	100.0	53	6	AR098682 AR098682 Sequence
	84	10	100.0	53	6	AR098683 AR098683 Sequence
c	85	10	100.0	53	6	AR204756 AR204756 Sequence
	86	10	100.0	53	6	AR204757 AR204757 Sequence
c	87	10	100.0	54	6	AR134108 AR134108 Sequence
c	88	10	100.0	54	6	AR134285 AR134285 Sequence
	89	10	100.0	57	8	ATH505724 AJ505724 Arabidops
c	90	10	100.0	58	8	ATH527067 AJ527067 Arabidops
	91	10	100.0	61	6	AX270701 AX270701 Sequence
	92	10	100.0	61	6	AX272232 AX272232 Sequence
	93	10	100.0	65	6	AX482835 AX482835 Sequence
	94	10	100.0	65	6	AX482852 AX482852 Sequence
	95	10	100.0	65	6	AX485490 AX485490 Sequence
	96	10	100.0	70	6	A81696 A81696 Sequence 1
	97	10	100.0	70	6	AR207788 AR207788 Sequence
	98	10	100.0	71	6	I62432 I62432 Sequence 5
	99	10	100.0	71	9	AH006998S06 AF026858 Homo sapi
c	100	10	100.0	73	6	BD055583 BD055583 Sequence
c	101	10	100.0	75	6	I62433 I62433 Sequence 6
	102	10	100.0	76	6	AX463283 AX463283 Sequence
	103	10	100.0	76	6	BD038896 BD038896 Sequence
	104	10	100.0	78	6	I62446 I62446 Sequence 19
	105	10	100.0	80	11	BX000934 BX000934 Arabidops
	106	10	100.0	81	14	AB015322 AB015322 Hepatitis
	107	10	100.0	81	14	AF148872 AF148872 Norwalk-l
	108	10	100.0	81	14	AF148873 AF148873 Norwalk-l
c	109	10	100.0	82	6	I62447 I62447 Sequence 20
	110	10	100.0	83	6	AX386001 AX386001 Sequence
	111	10	100.0	83	6	BD037643 BD037643 Sequence
	112	10	100.0	83	6	BD112411 BD112411 EST and e
	113	10	100.0	86	6	AX240905 AX240905 Sequence
	114	10	100.0	86	11	DM173H11S Z32462 D. melanoga
c	115	10	100.0	88	11	BX295958 BX295958 Arabidops
c	116	10	100.0	88	11	G66316 G66316 sY2268 YAC
c	117	10	100.0	91	3	DME426842 AJ426842 Drosophil
c	118	10	100.0	93	6	AR126785 AR126785 Sequence
c	119	10	100.0	93	6	AR202442 AR202442 Sequence
	120	10	100.0	93	6	AX522948 AX522948 Sequence
c	121	10	100.0	95	6	BD118772 BD118772 EST and e
c	122	10	100.0	98	8	YSCPIPRA M11711 Yeast RNA p
	123	10	100.0	98	10	RNPCTP5 AF040266 Rattus no
	124	10	100.0	99	6	BD038421 BD038421 Sequence
	125	10	100.0	99	6	BD038552 BD038552 Sequence
	126	10	100.0	102	11	G20394 G20394 human STS A
	127	10	100.0	103	8	OSA532497 AJ532497 Oryza sat
c	128	10	100.0	103	9	HSTEE4TF1 X84366 H.sapiens t
c	129	10	100.0	103	11	G19611 G19611 human STS A
c	130	10	100.0	104	6	AX645544 AX645544 Sequence
c	131	10	100.0	104	6	AX676705 AX676705 Sequence
c	132	10	100.0	104	6	BD049479 BD049479 Sequence
	133	10	100.0	104	8	AY220694 AY220694 Oryza sat
	134	10	100.0	105	6	AX127420 AX127420 Sequence
c	135	10	100.0	105	11	BX248221 BX248221 Arabidops
	136	10	100.0	105	11	G71016 G71016 A09121234FB
	137	10	100.0	107	9	HUMHELAC D45428 Homo sapien
	138	10	100.0	110	11	BX295578 BX295578 Arabidops
c	139	10	100.0	111	11	BX295946 BX295946 Arabidops
c	140	10	100.0	112	9	HS10B7R Z56291 H.sapiens C
c	141	10	100.0	113	8	ATH526836 AJ526836 Arabidops
c	142	10	100.0	113	8	ATH526837 AJ526837 Arabidops
c	143	10	100.0	116	9	HS197G4R Z55121 H.sapiens C
c	144	10	100.0	117	9	HS68D7R Z65938 H.sapiens C
	145	10	100.0	117	9	HS68E6F Z55835 H.sapiens C
c	146	10	100.0	118	6	AX554775 AX554775 Sequence
c	147	10	100.0	118	11	HSPE39G05 AL009929 H.sapiens
c	148	10	100.0	120	9	HUMIFARE M11287 Human alpha
	149	10	100.0	120	11	HUMSWX752 L24631 Human chrom
	150	10	100.0	121	6	AX262806 AX262806 Sequence
c	151	10	100.0	121	6	AX262807 AX262807 Sequence
	152	10	100.0	121	6	AX262822 AX262822 Sequence
c	153	10	100.0	121	6	AX262823 AX262823 Sequence
	154	10	100.0	121	6	AX262926 AX262926 Sequence
c	155	10	100.0	121	6	AX262927 AX262927 Sequence
	156	10	100.0	121	6	AX262930 AX262930 Sequence
c	157	10	100.0	121	6	AX262931 AX262931 Sequence
	158	10	100.0	121	8	AY201631 AY201631 Arabidops
	159	10	100.0	121	11	G32506 G32506 A009F19 Hum
	160	10	100.0	122	11	G43213 G43213 WIAF-1715-S
	161	10	100.0	122	11	G43214 G43214 WIAF-1716-S
	162	10	100.0	125	6	BD033545 BD033545 Sequence
c	163	10	100.0	128	1	HEA71U M33452 H.influenza
c	164	10	100.0	129	4	OAU35059 U35059 Ovis aries
	165	10	100.0	129	11	G32708 G32708 A009O27 Hum
	166	10	100.0	130	8	ATH505656 AJ505656 Arabidops
	167	10	100.0	130	8	ATH528046 AJ528046 Arabidops
c	168	10	100.0	130	9	HS191F10R Z57722 H.sapiens C
	169	10	100.0	130	9	HS191F9F Z65038 H.sapiens C
c	170	10	100.0	130	11	G18970 G18970 cow STS BMS
c	171	10	100.0	131	11	HUMSWX53 L14998 Human chrom
c	172	10	100.0	134	9	HSPA13A8 Z78634 H.sapiens f
	173	10	100.0	135	8	AF503161 AF503161 Ceiba pen
	174	10	100.0	135	10	MUSNR2C06 L35019 Mouse N-met
c	175	10	100.0	136	6	AX135409 AX135409 Sequence
c	176	10	100.0	136	11	HSPE56A10 AL034100 H.sapiens
	177	10	100.0	138	6	BD048886 BD048886 Sequence
	178	10	100.0	138	6	BD061135 BD061135 Secreted
c	179	10	100.0	138	9	HSPA15A11 Z78713 H.sapiens f
c	180	10	100.0	138	11	HUMUT799A L39147 Human STS U
c	181	10	100.0	140	9	HUMHELAD D45429 Homo sapien
c	182	10	100.0	140	11	G20401 G20401 human STS A
	183	10	100.0	141	6	BD055897 BD055897 Sequence
	184	10	100.0	144	11	AU046839 AU046839 Rattus no
c	185	10	100.0	145	9	AY190094 AY190094 Homo sapi
c	186	10	100.0	146	6	AR139657 AR139657 Sequence
	187	10	100.0	146	11	G02302 G02302 human STS S
	188	10	100.0	147	3	AF320603 AF320603 Trigona c
c	189	10	100.0	147	6	AX379108 AX379108 Sequence
c	190	10	100.0	147	6	BD046874 BD046874 Sequence
	191	10	100.0	147	9	AF515842 AF515842 Homo sapi
	192	10	100.0	148	6	BD043676 BD043676 Sequence
	193	10	100.0	148	6	BD043896 BD043896 Sequence
c	194	10	100.0	148	9	AY190090 AY190090 Homo sapi
	195	10	100.0	148	9	HUMFCGRA02 M90722 Human Fc-ga
c	196	10	100.0	149	6	AX259898 AX259898 Sequence
	197	10	100.0	149	9	HS59F11R Z61827 H.sapiens C
	198	10	100.0	150	11	G59542 G59542 SHGC-130099
	199	10	100.0	150	11	G59725 G59725 SHGC-130478
c	200	10	100.0	151	9	AY190102 AY190102 Homo sapi
	201	10	100.0	152	6	BD028580 BD028580 Sequence
c	202	10	100.0	152	9	AY190114 AY190114 Homo sapi
c	203	10	100.0	152	9	HUMALURPTF M37552 Human AFP g
	204	10	100.0	153	5	AY269268 AY269268 Gila eleg
c	205	10	100.0	153	9	HSXPAA4B X92876 H.sapiens m
	206	10	100.0	153	11	G64362 G64362 P316I19/T7
c	207	10	100.0	156	6	AX435756 AX435756 Sequence
c	208	10	100.0	156	9	HSA276202 AJ276202 Homo sapi
c	209	10	100.0	156	11	G30715 G30715 sWSS3438 Er
c	210	10	100.0	156	17	HSTEB0301 X85348 H.sapiens t
	211	10	100.0	157	6	AX196537 AX196537 Sequence

212	10	100.0	159	6	BD029565	BD029565 Sequence
c 213	10	100.0	159	9	HSA405777	AJ405777 Homo sapi
214	10	100.0	160	4	BTU43029	U43029 Bos taurus
215	10	100.0	160	10	AY054368	AY054368 Microtus
216	10	100.0	161	6	AX071949	AX071949 Sequence
217	10	100.0	161	10	AY054346	AY054346 Microtus
218	10	100.0	162	5	AF127383	AF127383 Melospiza
219	10	100.0	162	6	BD045865	BD045865 Sequence
c 220	10	100.0	162	9	HSA276200	AJ276200 Homo sapi
c 221	10	100.0	162	9	HSA276201	AJ276201 Homo sapi
c 222	10	100.0	162	9	HSA276203	AJ276203 Homo sapi
c 223	10	100.0	163	6	AX522866	AX522866 Sequence
224	10	100.0	164	9	HUMTAUC	L77209 Homo sapien
c 225	10	100.0	165	9	HSA276196	AJ276196 Homo sapi
c 226	10	100.0	165	9	HSA276199	AJ276199 Homo sapi
227	10	100.0	165	10	MUSMLCAF5	M20772 Mouse atria
228	10	100.0	167	11	DM146F11T	Z71094 D. melanoga
c 229	10	100.0	168	9	HSA276198	AJ276198 Homo sapi
230	10	100.0	169	6	A74774	A74774 Sequence 46
231	10	100.0	169	6	A77753	A77753 Sequence 46
232	10	100.0	169	6	AX198291	AX198291 Sequence
233	10	100.0	169	6	AX208855	AX208855 Sequence
c 234	10	100.0	169	9	HS140B8R	Z59286 H.sapiens C
c 235	10	100.0	169	11	G18626	G18626 BMS1167 cow
236	10	100.0	170	3	AF076879	AF076879 Trypanoso
c 237	10	100.0	170	8	ATH531773	AJ531773 Arabidops
238	10	100.0	170	9	HS140B8F	Z59285 H.sapiens C
c 239	10	100.0	172	6	BD050427	BD050427 Sequence
c 240	10	100.0	172	9	HS155E12F	Z59438 H.sapiens C
c 241	10	100.0	173	17	HSMC35A03	X88129 H.sapiens D
c 242	10	100.0	175	8	ATH528428	AJ528428 Arabidops
243	10	100.0	175	11	AL773189	AL773189 Arabidops
c 244	10	100.0	176	6	BD051623	BD051623 Sequence
c 245	10	100.0	176	11	HS362G17B	AL355239 H.sapiens
246	10	100.0	177	14	APHSPRH	M31582 Foot-and-mo
c 247	10	100.0	178	8	YSCRGIH1	K01052 Yeast (s.ce
248	10	100.0	178	11	AL773188	AL773188 Arabidops
249	10	100.0	178	11	HUMC5133	L28219 Human chrom
250	10	100.0	179	11	G43097	G43097 WIAF-1573-S
c 251	10	100.0	179	11	G70702	G70702 VE0208311FB
c 252	10	100.0	180	3	AF171818	AF171818 Drosophil
253	10	100.0	180	5	ASE287397	AJ287397 Acrocepha
254	10	100.0	180	11	G60685	G60685 SHGC-63256
255	10	100.0	181	6	AX196580	AX196580 Sequence
256	10	100.0	182	6	AX331451	AX331451 Sequence
257	10	100.0	183	3	DDU63603	U63603 Dictyosteli
c 258	10	100.0	183	8	YSCSPT7A	M87651 Saccharomyc
c 259	10	100.0	183	9	S67474S9	S67527 (GC*IS)=vit
c 260	10	100.0	183	9	SOU61050	U61050 Saguinus oe
c 261	10	100.0	184	6	AX202118	AX202118 Sequence
262	10	100.0	184	8	SGU011283	AJ011283 Stylosant
263	10	100.0	184	11	G07298	G07298 human STS W
c 264	10	100.0	185	8	ATH527680	AJ527680 Arabidops
c 265	10	100.0	185	8	ATH527682	AJ527682 Arabidops
266	10	100.0	186	6	AX251610	AX251610 Sequence
c 267	10	100.0	186	9	AY239354	AY239354 Homo sapi
268	10	100.0	186	11	G18667	G18667 BMS1385 cow
269	10	100.0	187	4	PIGCGT8	M97235 Pig (clone
c 270	10	100.0	187	6	BD043228	BD043228 Sequence
271	10	100.0	188	8	AB063552	AB063552 Fagus jap
272	10	100.0	188	8	AB063553	AB063553 Fagus cre
c 273	10	100.0	189	4	AF201741S2	AF201742 Bos tauru
c 274	10	100.0	189	6	BD040269	BD040269 Sequence
c 275	10	100.0	189	8	ATH522519	AJ522519 Arabidops
276	10	100.0	191	6	BD028450	BD028450 Sequence
277	10	100.0	191	9	HS62A8F	Z55754 H.sapiens C
c 278	10	100.0	191	11	G32336	G32336 A006E46 Hum
c 279	10	100.0	192	9	HUMTCRBY	L34725 Homo sapien
c 280	10	100.0	193	6	AX047793	AX047793 Sequence
c 281	10	100.0	193	11	BX295948	BX295948 Arabidops
c 282	10	100.0	194	6	AX452433	AX452433 Sequence
c 283	10	100.0	194	6	BD046891	BD046891 Sequence
284	10	100.0	194	11	AF041417	AF041417 Trypanoso
285	10	100.0	194	11	G12787	G12787 sWSS2144 Er
286	10	100.0	195	6	BD050159	BD050159 Sequence
c 287	10	100.0	195	11	BX293660	BX293660 Arabidops
288	10	100.0	195	11	G32866	G32866 A009V05 Hum
289	10	100.0	196	1	ECU35065	U35065 Escherichia
c 290	10	100.0	196	9	HS87B3F	Z63570 H.sapiens C
291	10	100.0	196	9	HS87B3R	Z63571 H.sapiens C
c 292	10	100.0	196	11	BX294583	BX294583 Arabidops
293	10	100.0	197	6	AX186932	AX186932 Sequence
c 294	10	100.0	197	6	I01679	I01679 Sequence 4
c 295	10	100.0	198	6	AX202139	AX202139 Sequence
296	10	100.0	198	6	AX311050	AX311050 Sequence
c 297	10	100.0	198	9	HSA405781	AJ405781 Homo sapi
298	10	100.0	199	6	BD030797	BD030797 Sequence
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300	10	100.0	200	11	BV012598	BV012598 M6S151 Hu
301	10	100.0	201	6	AX173101	AX173101 Sequence
c 302	10	100.0	201	6	AX276551	AX276551 Sequence
c 303	10	100.0	201	6	AX435807	AX435807 Sequence
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c 306	10	100.0	201	9	HSA405788	AJ405788 Homo sapi
c 307	10	100.0	202	5	AY029202	AY029202 Gallus ga
c 308	10	100.0	203	3	AY185121	AY185121 Leishmani
309	10	100.0	203	3	LSP270148	AJ270148 Leishmani
310	10	100.0	203	9	AF262665	AF262665 Homo sapi
c 311	10	100.0	203	11	G20532	G20532 human STS A
312	10	100.0	204	6	BD042756	BD042756 Sequence
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c 314	10	100.0	204	9	HSA405762	AJ405762 Homo sapi
315	10	100.0	204	10	MMIG7F1A	X55507 M.musculus
c 316	10	100.0	204	11	G20705	G20705 human STS A
c 317	10	100.0	205	6	AX387628	AX387628 Sequence
318	10	100.0	205	9	HUMGMP1405	M60223 Human granu
319	10	100.0	206	6	AR251645	AR251645 Sequence
320	10	100.0	206	8	ATH551904	AJ551904 Arabidops
c 321	10	100.0	206	10	AF361008	AF361008 Mus muscu
322	10	100.0	207	8	AB043755	AB043755 Fagus cre
323	10	100.0	207	8	AB043756	AB043756 Fagus cre
324	10	100.0	207	9	HSA011594	AJ011594 Homo sapi
c 325	10	100.0	207	9	HSA300410	AJ300410 Homo sapi
326	10	100.0	208	6	AX310754	AX310754 Sequence
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c 328	10	100.0	208	11	AF235213	AF235213 Sus scrof
329	10	100.0	209	3	LSP270149	AJ270149 Leishmani
c 330	10	100.0	210	6	AX415513	AX415513 Sequence
c 331	10	100.0	210	6	AX431292	AX431292 Sequence
c 332	10	100.0	210	9	HSA405856	AJ405856 Homo sapi
333	10	100.0	212	6	AX482093	AX482093 Sequence
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335	10	100.0	212	6	AX721693	AX721693 Sequence
336	10	100.0	212	6	BD045031	BD045031 Sequence
337	10	100.0	212	9	HSATP7A10	U27369 Human Menke
338	10	100.0	213	6	BD028873	BD028873 Sequence
c 339	10	100.0	213	6	BD053618	BD053618 Sequence
c 340	10	100.0	213	9	HSA405752	AJ405752 Homo sapi
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343	10	100.0	215	1	WSP428343	AJ428343 Wolbachia
344	10	100.0	216	1	RPZ82717	Z82717 R.prowazeki
c 345	10	100.0	216	3	CECEH11H	X52813 Caenorhabdi
c 346	10	100.0	216	3	LEIREPAC	L42477 Leishmania
c 347	10	100.0	216	3	LEIREPAE	L42479 Leishmania
c 348	10	100.0	216	3	LEIREPAH	L42482 Leishmania
c 349	10	100.0	216	3	LEIREPAI	L42483 Leishmania
c 350	10	100.0	216	3	LEIREPAL	L42486 Leishmania
c 351	10	100.0	216	3	LEIREPAW	L42497 Leishmania
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c 353	10	100.0	216	9	HSA389990	AJ389990 Homo sapi
c 354	10	100.0	216	9	HSA405768	AJ405768 Homo sapi
c 355	10	100.0	216	9	HUMTCRBU	L34724 Homo sapien
356	10	100.0	216	10	AF526122	AF526122 Peromyscu
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359	10	100.0	217	6	BD055876	BD055876 Sequence
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c 361	10	100.0	217	11	G04642	G04642 human STS W
362	10	100.0	218	6	BD056063	BD056063 Sequence
363	10	100.0	218	9	HSTNFR2S07	U52162 Human tumor
364	10	100.0	218	10	MMU409500	AJ409500 Mus muscu
c 365	10	100.0	219	1	STRMLIKEB	L05018 Streptococc
c 366	10	100.0	219	3	AF323685	AF323685 Acropora
c 367	10	100.0	219	9	HS184A2F	Z55009 H.sapiens C
368	10	100.0	219	11	HSPE17F08	AL009571 H.sapiens
369	10	100.0	220	8	AY200757	AY200757 Arabidops
370	10	100.0	221	9	HUMENKB1	K02267 Human enkep
c 371	10	100.0	221	11	G35200	G35200 cre12e Cryp
c 372	10	100.0	222	9	HSA405857	AJ405857 Homo sapi
c 373	10	100.0	222	9	HUMTCRBAI	L34731 Homo sapien
c 374	10	100.0	222	9	HUMTCRBAN	L34736 Homo sapien
375	10	100.0	222	14	U96350	U96350 Hepatitis G
c 376	10	100.0	223	6	BD032653	BD032653 Sequence
c 377	10	100.0	223	8	AY032840	AY032840 Passiflor
378	10	100.0	223	11	G26013	G26013 human STS E
379	10	100.0	223	14	U96357	U96357 Hepatitis G
c 380	10	100.0	224	8	AY017798	AY017798 Oryza sat
381	10	100.0	224	8	AY020653	AY020653 Oryza sat
c 382	10	100.0	224	8	AY023853	AY023853 Oryza sat
383	10	100.0	225	6	BD033343	BD033343 Sequence
384	10	100.0	225	8	AF374108	AF374108 Fusarium
385	10	100.0	225	8	AY077694	AY077694 Cantharel
c 386	10	100.0	225	9	HS30A2R	Z55278 H.sapiens C
c 387	10	100.0	225	9	HSA403790	AJ403790 Homo sapi
388	10	100.0	226	6	BD071601	BD071601 Secreted
c 389	10	100.0	226	8	AY017699	AY017699 Oryza sat
c 390	10	100.0	226	8	AY017828	AY017828 Oryza sat
391	10	100.0	226	8	AY019941	AY019941 Oryza sat
c 392	10	100.0	226	8	AY212115	AY212115 Triticum
c 393	10	100.0	226	11	AU026388	AU026388 Rattus no
394	10	100.0	226	11	AU048388	AU048388 Rattus no
c 395	10	100.0	226	11	G02977	G02977 human STS W
396	10	100.0	226	11	G05222	G05222 human STS W
397	10	100.0	226	11	HSA296842	AJ296842 Homo sapi
398	10	100.0	227	8	AB043754	AB043754 Fagus cre
399	10	100.0	227	8	AY023637	AY023637 Oryza sat
c 400	10	100.0	227	10	RNW3PDE03	U01283 Rattus norv
c 401	10	100.0	227	11	G05891	G05891 human STS W
c 402	10	100.0	228	6	AR269536	AR269536 Sequence
c 403	10	100.0	228	6	AX437220	AX437220 Sequence
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c 405	10	100.0	228	8	AY018284	AY018284 Oryza sat
c 406	10	100.0	228	8	AY024236	AY024236 Oryza sat
c 407	10	100.0	228	9	HSA230068	AJ230068 Homo sapi
c 408	10	100.0	228	9	HSA405674	AJ405674 Homo sapi
c 409	10	100.0	228	9	HSA405793	AJ405793 Homo sapi
410	10	100.0	228	11	G67231	G67231 csnpku86-pc
c 411	10	100.0	229	9	HSCTL40	X51790 Human mRNA
412	10	100.0	229	11	AU027640	AU027640 Rattus no
413	10	100.0	230	8	AY022834	AY022834 Oryza sat
c 414	10	100.0	230	9	HSA230081	AJ230081 Homo sapi
c 415	10	100.0	230	9	HSA403861	AJ403861 Homo sapi
416	10	100.0	231	6	AX184629	AX184629 Sequence
c 417	10	100.0	231	8	HFI311824	AJ311824 Halopteri
c 418	10	100.0	231	9	HSCTL212	X51788 Human mRNA
c 419	10	100.0	232	6	BD117604	BD117604 EST and e
420	10	100.0	232	8	AF374120	AF374120 Fusarium
c 421	10	100.0	233	6	BD139321	BD139321 Extended
c 422	10	100.0	233	9	HSA389986	AJ389986 Homo sapi
c 423	10	100.0	233	9	HSCTL67	X51794 Human mRNA
c 424	10	100.0	233	11	G13001	G13001 sWSS2840 Er
c 425	10	100.0	234	3	CE3	X17075 Caenorhabdi
c 426	10	100.0	234	9	HSA405685	AJ405685 Homo sapi
c 427	10	100.0	235	5	GGZ94830	Z94830 G.gallus mi
c 428	10	100.0	235	8	AY032838	AY032838 Passiflor
429	10	100.0	235	10	AF308440	AF308440 Mus muscu
430	10	100.0	236	8	AB043751	AB043751 Fagus cre
431	10	100.0	236	8	AB043752	AB043752 Fagus cre
432	10	100.0	236	8	AB043753	AB043753 Fagus cre
433	10	100.0	236	8	AB043757	AB043757 Fagus cre
434	10	100.0	236	8	AB043758	AB043758 Fagus cre
435	10	100.0	236	8	AB043759	AB043759 Fagus cre
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437	10	100.0	236	8	AB043761	AB043761 Fagus jap
438	10	100.0	236	8	AB043762	AB043762 Fagus jap
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440	10	100.0	236	8	AB066498	AB066498 Fagus gra
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443	10	100.0	236	8	AY022309	AY022309 Oryza sat
c 444	10	100.0	237	1	AF093626	AF093626 Bacillus
c 445	10	100.0	237	5	GGZ94841	Z94841 G.gallus mi
446	10	100.0	237	9	HS55G9R	Z65737 H.sapiens C
c 447	10	100.0	237	9	HSU39128	U39128 Homo sapien
c 448	10	100.0	237	9	HUMDINUCRP	M94958 Human dinuc
c 449	10	100.0	238	6	AX094172	AX094172 Sequence
c 450	10	100.0	238	11	G63246	G63246 SHGC-140885
c 451	10	100.0	239	5	GGZ94829	Z94829 G.gallus mi
c 452	10	100.0	239	6	BD028893	BD028893 Sequence
453	10	100.0	239	6	BD048305	BD048305 Sequence
c 454	10	100.0	239	6	BD059663	BD059663 Secreted
455	10	100.0	239	8	AB084875	AB084875 Schizosac
c 456	10	100.0	239	11	G04386	G04386 human STS W
457	10	100.0	240	6	BD071286	BD071286 Secreted
458	10	100.0	240	8	AY021176	AY021176 Oryza sat
c 459	10	100.0	240	9	AF041219	AF041219 Homo sapi
460	10	100.0	240	9	F267517S12	AF267528 Homo sapi
c 461	10	100.0	240	9	HSA405839	AJ405839 Homo sapi
c 462	10	100.0	240	9	S63249	S63249 T-cell rece
463	10	100.0	240	11	AU025673	AU025673 Rattus no
c 464	10	100.0	241	5	GGZ95323	Z95323 G.gallus mi
465	10	100.0	241	6	AR240300	AR240300 Sequence
466	10	100.0	241	6	AR280852	AR280852 Sequence
467	10	100.0	241	6	AR283348	AR283348 Sequence
468	10	100.0	241	6	AX303040	AX303040 Sequence
469	10	100.0	242	8	AY017747	AY017747 Oryza sat
470	10	100.0	242	9	HS46F12R	Z58627 H.sapiens C
c 471	10	100.0	243	6	AX048534	AX048534 Sequence
472	10	100.0	243	11	G36317	G36317 STS h14a250
c 473	10	100.0	244	9	HS13B3F	Z56737 H.sapiens C
474	10	100.0	245	8	AF374129	AF374129 Fusarium
c 475	10	100.0	245	9	HSA403843	AJ403843 Homo sapi
c 476	10	100.0	245	11	AL823657	AL823657 Arabidops
477	10	100.0	245	11	HSA121XD5	Z52141 H.sapiens (
478	10	100.0	246	6	AX185506	AX185506 Sequence
c 479	10	100.0	246	9	HS13B2F	Z54602 H.sapiens C
c 480	10	100.0	246	9	HSA405738	AJ405738 Homo sapi
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c 482	10	100.0	246	11	G49085	G49085 SHGC-83039
c 483	10	100.0	247	6	AR270174	AR270174 Sequence
484	10	100.0	247	6	BD043817	BD043817 Sequence
c 485	10	100.0	247	8	AF068738	AF068738 Kluyverom
c 486	10	100.0	248	8	AY018030	AY018030 Oryza sat
487	10	100.0	249	8	AF374103	AF374103 Fusarium
488	10	100.0	249	8	AF374104	AF374104 Fusarium
489	10	100.0	249	8	AF374105	AF374105 Fusarium
490	10	100.0	249	8	AF374106	AF374106 Fusarium
491	10	100.0	249	8	AF374107	AF374107 Fusarium
492	10	100.0	249	8	AF374109	AF374109 Fusarium
493	10	100.0	249	8	AF374110	AF374110 Fusarium
494	10	100.0	249	8	AF374111	AF374111 Fusarium
495	10	100.0	249	8	AF374112	AF374112 Fusarium
496	10	100.0	249	8	AF374113	AF374113 Fusarium
497	10	100.0	249	8	AF374114	AF374114 Fusarium
498	10	100.0	249	8	AF374115	AF374115 Fusarium
499	10	100.0	249	8	AF374116	AF374116 Fusarium
500	10	100.0	249	8	AF374117	AF374117 Fusarium

ALIGNMENTS

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RESULT 1
BD065135
LOCUS       BD065135                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065135
VERSION     BD065135.1  GI:22610738
KEYWORDS    JP 2001509017-A/71.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 71 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/71
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES             Location/Qualifiers
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Qy          1 CTTCTCTTTT 10
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Db          1 CTTCTCTTTT 10


RESULT 2
AR029992/c
LOCUS       AR029992                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 181 from patent US 5861244.
ACCESSION   AR029992
VERSION     AR029992.1  GI:5943206
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 181 19-JAN-1999;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        8 a      0 c      4 g      0 t
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  Query Match             100.0%;  Score 10;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 3
AR030057
LOCUS       AR030057                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 246 from patent US 5861244.
ACCESSION   AR030057
VERSION     AR030057.1  GI:5943271
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 246 19-JAN-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        0 a      4 c      0 g      8 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          3 CTTCTCTTTT 12


RESULT 4
AX500413/c
LOCUS       AX500413                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1720 from Patent EP1229046.
ACCESSION   AX500413
VERSION     AX500413.1  GI:23382706
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1720 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT        8 a      0 c      7 g      2 t
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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 5
AX500414/c
LOCUS       AX500414                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1721 from Patent EP1229046.
ACCESSION   AX500414
VERSION     AX500414.1  GI:23382707
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
  AUTHORS  Zhan,J.
  TITLE    Human testis expressed patched like protein
  JOURNAL  Patent: EP 1229046-A 1721 07-AUG-2002;
           Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
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BASE COUNT        8 a      0 c      6 g      3 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 17;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 6
AX500415/c
LOCUS       AX500415                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1722 from Patent EP1229046.
ACCESSION   AX500415
VERSION     AX500415.1  GI:23382708
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1722 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      0 c      5 g      3 t
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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 7
AX500416/c
LOCUS       AX500416                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1723 from Patent EP1229046.
ACCESSION   AX500416
VERSION     AX500416.1  GI:23382709
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1723 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      0 c      6 g      3 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 8
AX500417/c
LOCUS       AX500417                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1724 from Patent EP1229046.
ACCESSION   AX500417
VERSION     AX500417.1  GI:23382710
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1724 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      0 c      6 g      3 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 9
AX500418/c
LOCUS       AX500418                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1725 from Patent EP1229046.
ACCESSION   AX500418
VERSION     AX500418.1  GI:23382711
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1725 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      1 c      5 g      3 t
ORIGIN
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  Query Match            100.0%;  Score 10;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 10
AX500419/c
LOCUS       AX500419                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1726 from Patent EP1229046.
ACCESSION   AX500419
VERSION     AX500419.1  GI:23382712
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1726 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      1 c      4 g      4 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 11
AX500420/c
LOCUS       AX500420                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1727 from Patent EP1229046.
ACCESSION   AX500420
VERSION     AX500420.1  GI:23382713
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1727 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      1 c      5 g      3 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 12
AX673153
LOCUS       AX673153                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1598 from Patent WO03004526.
ACCESSION   AX673153
VERSION     AX673153.1  GI:29331501
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1598 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      6 c      1 g      8 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          6 CTTCTCTTTT 15


RESULT 13
AX659410
LOCUS       AX659410                  19 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 12 from Patent WO02102824.
ACCESSION   AX659410
VERSION     AX659410.1  GI:29161640
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beimfohr,C. and Snaidr,J.
  TITLE     Method for specific fast detection of relevant bacteria in drinking
            water
  JOURNAL   Patent: WO 02102824-A 12 27-DEC-2002;
            Vermicon AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        1 a      7 c      2 g      9 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          4 CTTCTCTTTT 13


RESULT 14
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AR315845/c
LOCUS       AR315845                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6382 from patent US 6559294.
ACCESSION   AR315845
VERSION     AR315845.1  GI:31709271
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6382 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        8 a      4 c      4 g      4 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 15
I48976
LOCUS       I48976                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5627054.
ACCESSION   I48976
VERSION     I48976.1  GI:2467439
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Gillespie,D. deceased.
  TITLE     Competitor primer asymmetric polymerase chain reaction
  JOURNAL   Patent: US 5627054-A 3 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      5 c      3 g      8 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 16
AR054595/c
LOCUS       AR054595                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5837447.
ACCESSION   AR054595
VERSION     AR054595.1  GI:5980172
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Gorski,J.
  TITLE     Monitoring an immune response by analysis of amplified
            immunoglobulin or T-cell-receptor nucleic acid
  JOURNAL   Patent: US 5837447-A 16 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        8 a      3 c      7 g      3 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 17
AR136775/c
LOCUS       AR136775                 21 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 8 from patent US 6162435.
ACCESSION   AR136775
VERSION     AR136775.1  GI:14478025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Minion,F.Chris. and Hsu,T.
  TITLE     Recombinant mycoplasma hyopneumoniae vaccine
  JOURNAL   Patent: US 6162435-A 8 19-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT       12 a      0 c      7 g      2 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 18
E35992/c
LOCUS       E35992                   21 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for detecting Kawasaki disease factor.
ACCESSION   E35992
VERSION     E35992.1  GI:18624703
KEYWORDS    JP 2000157297-A/83.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Yoshioka,T. and Suzuki,R.
  TITLE     Method for detecting Kawasaki disease factor
  JOURNAL   Patent: JP 2000157297-A 83 13-JUN-2000;
            SHIONOGI & CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000157297-A/83
            PD   13-JUN-2000
            PF   01-DEC-1998 JP 1998341661
            PR
            PI   TAKESHI YOSHIOKA,RYUJI SUZUKI
            PC   C12Q1/68,C12N15/09,G01N33/48,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT         8 a      3 c      7 g      3 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 19
AR029876
LOCUS       AR029876                 22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 65 from patent US 5861244.
ACCESSION   AR029876
VERSION     AR029876.1  GI:5943090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 65 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
BASE COUNT         1 a      5 c      0 g     16 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          6 CTTCTCTTTT 15


RESULT 20
AX352316
LOCUS       AX352316                 22 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 612 from Patent WO0193902.
ACCESSION   AX352316
VERSION     AX352316.1  GI:18617599
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 612 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
BASE COUNT         1 a      4 c      3 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 21
AX352317
LOCUS       AX352317                 22 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 613 from Patent WO0193902.
ACCESSION   AX352317
VERSION     AX352317.1  GI:18617600
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 613 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
BASE COUNT         1 a      4 c      4 g     13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 22
AX352318
LOCUS       AX352318                 22 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 614 from Patent WO0193902.
ACCESSION   AX352318
VERSION     AX352318.1  GI:18617601
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 614 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
BASE COUNT         1 a      4 c      2 g     15 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 23
AR069183/c
LOCUS       AR069183                 24 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 17 from patent US 5891623.
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```
ACCESSION   AR069183
VERSION     AR069183.1  GI:7220071
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Primi,D.
  TITLE     Diagnosis and treatment of AIDS onset
  JOURNAL   Patent: US 5891623-A 17 06-APR-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT       10 a      3 c      7 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 24
AR102693/c
LOCUS       AR102693                  24 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 16 from patent US 6087096.
ACCESSION   AR102693
VERSION     AR102693.1  GI:12814281
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dau,P.C. and Liu,D.
  TITLE     Method of intrafamily fragment analysis of the T cell receptor
            .alpha. and .beta. chain CDR3 regions
  JOURNAL   Patent: US 6087096-A 16 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT       10 a      3 c      7 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 25
AR175558/c
LOCUS       AR175558                  24 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6309837.
ACCESSION   AR175558
VERSION     AR175558.1  GI:17916857
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dean,R.A. and Wang,Y.-H.
  TITLE     PCR-based method for identifying a fusarium wilt-resistant genotype
            in plants
  JOURNAL   Patent: US 6309837-A 3 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT       14 a      1 c      8 g      1 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 26
AX443310/c
LOCUS       AX443310                  24 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 46 from Patent WO0216940.
ACCESSION   AX443310
VERSION     AX443310.1  GI:21690705
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sulavik,M., Ling,L.L., Opperman,T., Moir,D.T. and Bunker,C.
  TITLE     Genomics-assisted rapid identification of targets
  JOURNAL   Patent: WO 0216940-A 46 28-FEB-2002;
            Genome Therapeutics Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        9 a      4 c      6 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 27
BD090389/c
LOCUS       BD090389                  24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD090389
VERSION     BD090389.1  GI:22635999
KEYWORDS    JP 2001321190-A/2633.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2633 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2633
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
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FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT       12 a      2 c      6 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 28
BD176467/c
LOCUS       BD176467                  24 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  A method of arraying genome clone.
ACCESSION   BD176467
VERSION     BD176467.1  GI:29122175
KEYWORDS    WO 02072815-A/267.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: WO 02072815-A 267 19-SEP-2002;
            EIICHI SOEDA,TAKESHI KUKITA
COMMENT     OS   Artificial Sequence
            PN   WO 02072815-A/267
            PD   19-SEP-2002
            PF   17-MAY-2001 WO 2001JP004139
            PR   12-MAR-2001 JP 01P    68285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12Q1/68
            CC   Description of Artificial Sequence: Synthetic DNA FH   Key
                 Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT       12 a      2 c      6 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 29
I64401/c
LOCUS       I64401                    24 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 17 from patent US 5665355.
ACCESSION   I64401
VERSION     I64401.1  GI:2481295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Primi,D.
  TITLE     Diagnosis and treatment of AIDS onset
  JOURNAL   Patent: US 5665355-A 17 09-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT       10 a      3 c      7 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 30
AX502410/c
LOCUS       AX502410                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3717 from Patent EP1229046.
ACCESSION   AX502410
VERSION     AX502410.1  GI:23384703
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3717 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      2 c      9 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 31
AX502411/c
LOCUS       AX502411                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3718 from Patent EP1229046.
ACCESSION   AX502411
VERSION     AX502411.1  GI:23384704
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3718 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      2 c      9 g      6 t
ORIGIN
```

```
  Query Match            100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         24 CTTCTCTTTT 15


RESULT 32
AX502412/c
LOCUS       AX502412                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3719 from Patent EP1229046.
ACCESSION   AX502412
VERSION     AX502412.1  GI:23384705
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3719 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      2 c      9 g      5 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 33
AX502413/c
LOCUS       AX502413                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3720 from Patent EP1229046.
ACCESSION   AX502413
VERSION     AX502413.1  GI:23384706
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3720 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      2 c      9 g      5 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 34
AX502414/c
LOCUS       AX502414                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3721 from Patent EP1229046.
ACCESSION   AX502414
VERSION     AX502414.1  GI:23384707
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3721 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      2 c      8 g      6 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 35
AX502415/c
LOCUS       AX502415                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3722 from Patent EP1229046.
ACCESSION   AX502415
VERSION     AX502415.1  GI:23384708
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3722 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      2 c      8 g      6 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 36
AX502416/c
LOCUS       AX502416                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3723 from Patent EP1229046.
ACCESSION   AX502416
```

```
VERSION     AX502416.1  GI:23384709
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3723 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      1 c      8 g      7 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 37
AX502417/c
LOCUS       AX502417                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3724 from Patent EP1229046.
ACCESSION   AX502417
VERSION     AX502417.1  GI:23384710
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3724 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      1 c      9 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 38
AX502418/c
LOCUS       AX502418                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3725 from Patent EP1229046.
ACCESSION   AX502418
VERSION     AX502418.1  GI:23384711
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3725 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      2 c      9 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 39
AX502419/c
LOCUS       AX502419                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3726 from Patent EP1229046.
ACCESSION   AX502419
VERSION     AX502419.1  GI:23384712
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3726 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      8 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 40
AX502420/c
LOCUS       AX502420                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3727 from Patent EP1229046.
ACCESSION   AX502420
VERSION     AX502420.1  GI:23384713
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3727 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
```

```
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      7 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 41
AX502421/c
LOCUS       AX502421                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3728 from Patent EP1229046.
ACCESSION   AX502421
VERSION     AX502421.1  GI:23384714
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3728 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      7 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 42
AX502422/c
LOCUS       AX502422                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3729 from Patent EP1229046.
ACCESSION   AX502422
VERSION     AX502422.1  GI:23384715
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3729 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      7 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 43
AX502423/c
LOCUS       AX502423                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3730 from Patent EP1229046.
ACCESSION   AX502423
VERSION     AX502423.1  GI:23384716
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3730 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      3 c      7 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 44
AX502424/c
LOCUS       AX502424                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3731 from Patent EP1229046.
ACCESSION   AX502424
VERSION     AX502424.1  GI:23384717
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3731 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      4 c      6 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2
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RESULT 45
AX502425/c
LOCUS       AX502425                  25 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 3732 from Patent EP1229046.
ACCESSION   AX502425
VERSION     AX502425.1  GI:23384718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 3732 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        9 a      4 c      6 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 46
I48977
LOCUS       I48977                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5627054.
ACCESSION   I48977
VERSION     I48977.1  GI:2467440
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gillespie,D. deceased.
  TITLE     Competitor primer asymmetric polymerase chain reaction
  JOURNAL   Patent: US 5627054-A 4 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        4 a      5 c      3 g      8 t      5 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 47
ATH525492/c
LOCUS       ATH525492                 26 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            097H03.
ACCESSION   AJ525492
VERSION     AJ525492.1  GI:26793728
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 26)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="097H03"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .26
                     /note="T-DNA flanking sequence
                     left border"
BASE COUNT       13 a      3 c      4 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 8;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 48
ATH525503/c
LOCUS       ATH525503                 26 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            098B06.
ACCESSION   AJ525503
VERSION     AJ525503.1  GI:26793739
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 26)
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  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="098B06"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .26
                     /note="T-DNA flanking sequence
                     left border"
BASE COUNT       13 a      3 c      4 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 8;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 49
AR066258/c
LOCUS       AR066258                  27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 23 from patent US 5849900.
ACCESSION   AR066258
VERSION     AR066258.1  GI:5996474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Moelling,K.
  TITLE     Inhibition of viruses by antisense oligomers capable of binding to
            polypurine rich tract of single-stranded RNA or RNA-DNA hybrids
  JOURNAL   Patent: US 5849900-A 23 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        7 a      8 c      8 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 50
AR191561/c
LOCUS       AR191561                  27 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7049 from patent US 6346398.
ACCESSION   AR191561
VERSION     AR191561.1  GI:20237526
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7049 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT       12 a      1 c      9 g      4 t      1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         27 CTTCTCTTTT 18


RESULT 51
AX115839/c
LOCUS       AX115839                  27 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 962 from Patent WO0129262.
ACCESSION   AX115839
VERSION     AX115839.1  GI:14032781
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 962 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT       13 a      5 c      4 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 52
AX040823
LOCUS       AX040823                  28 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 16 from Patent WO0064930.
ACCESSION   AX040823
VERSION     AX040823.1  GI:11340462
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jay,G.D.
  TITLE     Tribonectins
  JOURNAL   Patent: WO 0064930-A 16 02-NOV-2000;
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           RHODE ISLAND HOSPITAL (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      7 c      6 g     10 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 21


RESULT 53
AR261655
LOCUS       AR261655                 29 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 133 from patent US 6322976.
ACCESSION   AR261655
VERSION     AR261655.1  GI:28072733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Aitman,T.J., Scott,J. and Stanton,L.W.
  TITLE     Compositions and methods of disease diagnosis and therapy
  JOURNAL   Patent: US 6322976-A 133 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        1 a      5 c     10 g     13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 54
AR261654
LOCUS       AR261654                 30 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 132 from patent US 6322976.
ACCESSION   AR261654
VERSION     AR261654.1  GI:28072732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Aitman,T.J., Scott,J. and Stanton,L.W.
  TITLE     Compositions and methods of disease diagnosis and therapy
  JOURNAL   Patent: US 6322976-A 132 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        1 a      5 c     10 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 55
AR261656
LOCUS       AR261656                 30 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 134 from patent US 6322976.
ACCESSION   AR261656
VERSION     AR261656.1  GI:28072734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Aitman,T.J., Scott,J. and Stanton,L.W.
  TITLE     Compositions and methods of disease diagnosis and therapy
  JOURNAL   Patent: US 6322976-A 134 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        1 a      5 c     10 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 56
AR261657
LOCUS       AR261657                 30 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 135 from patent US 6322976.
ACCESSION   AR261657
VERSION     AR261657.1  GI:28072735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Aitman,T.J., Scott,J. and Stanton,L.W.
  TITLE     Compositions and methods of disease diagnosis and therapy
  JOURNAL   Patent: US 6322976-A 135 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
BASE COUNT        1 a      5 c      9 g     15 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 57
AR120483/c
LOCUS       AR120483                 33 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 359 from patent US 6159469.
ACCESSION   AR120483
VERSION     AR120483.1  GI:14104059
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B.,
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            Fannon,M.R. and Rosen,C.A.
  TITLE     Streptococcus pneumoniae antigens and vaccines
  JOURNAL   Patent: US 6159469-A 359 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT       14 a      5 c      9 g      5 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 58
BD063492/c
LOCUS       BD063492                33 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Streptococcus pneumoniae antigens and vaccines.
ACCESSION   BD063492
VERSION     BD063492.1  GI:22609095
KEYWORDS    JP 2001505415-A/246.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kunsch,C.A., Choi,G.H., Johnson,S.L. and Hromockyj,A.
  TITLE     Streptococcus pneumoniae antigens and vaccines
  JOURNAL   Patent: JP 2001505415-A 246 24-APR-2001;
            HUMAN GENOME SCIENCES INC
COMMENT     PN   JP 2001505415-A/246
            PD   24-APR-2001
            PF   30-OCT-1997 JP 1998520667
            PR   31-OCT-1996 US    60/029960
            PI   CHARLES A KUNSCH,GIL H CHOI,SYDNOR L JOHNSON,ALEX HROMOCKYJ PC
              C12N15/31,C12N5/18,C12N1/21,C07K14/315,C12Q1/68,A61K39/09, PC
            G01N33/569,
            PC   G01N33/68
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       14 a      5 c      9 g      5 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 59
E36416
LOCUS       E36416                  33 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  dna G.
ACCESSION   E36416
VERSION     E36416.1  GI:13022642
KEYWORDS    JP 1999239489-A/3.
SOURCE      Streptococcus pneumoniae
  ORGANISM  Streptococcus pneumoniae
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Earl,W.M., Deborah,D.J., Ming,H., Richard,R.W. and Ana,R.R.
  TITLE     dna G
  JOURNAL   Patent: JP 1999239489-A 3 07-SEP-1999;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Streptococcus pneumoniae
            PN   JP 1999239489-A/3
            PD   07-SEP-1999
            PF   21-OCT-1998 JP 1998338366
            PR   21-OCT-1997 US    60/070912
            PI   EARL WILLIAM MEI,DEBORAH D JAWASUKI,MING HWANG, PI   RICHARD
            ROIDO WOREN,
            PI   ANA RISA RENOX
            PC   C12N15/09,A61K31/00,A61K31/70,A61K38/00,A61K39/00,A61K48/00,
            PC   C07K14/315,
            PC   C07K16/12,C12P21/02,G01N33/53//C12P21/08,C12N15/00,A61K37/02
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Streptococcus pneumoniae'.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Streptococcus pneumoniae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1313"
BASE COUNT        8 a      7 c      4 g     14 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 20


RESULT 60
AX218433/c
LOCUS       AX218433                38 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 3875 from Patent WO0159103.
ACCESSION   AX218433
VERSION     AX218433.1  GI:15546157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3875 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT       14 a      6 c     14 g      4 t
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 38;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 29


RESULT 61
AX220343
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LOCUS       AX220343                38 bp    mRNA    linear   PAT 07-SEP-2001
DEFINITION  Sequence 5785 from Patent WO0159103.
ACCESSION   AX220343
VERSION     AX220343.1  GI:15548067
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 5785 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
BASE COUNT        9 a     10 c      9 g     10 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         29 CTTCTCTTTT 38


RESULT 62
AX273375/c
LOCUS       AX273375                38 bp    mRNA    linear   PAT 29-OCT-2001
DEFINITION  Sequence 944 from Patent WO0162911.
ACCESSION   AX273375
VERSION     AX273375.1  GI:16546112
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
  TITLE     Method and reagent for the inhibition of grid
  JOURNAL   Patent: WO 0162911-A 944 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /note="Enzymatic Nucleic Acid"
BASE COUNT       11 a      6 c     13 g      8 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 29


RESULT 63
BD182426
LOCUS       BD182426                40 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Human artificial chromosomes comprising human antibody light chain
            lambda gene, and non-human animals retaining human artificial
            chromosome transmittable to progeny.
ACCESSION   BD182426
VERSION     BD182426.1  GI:30793344
KEYWORDS    WO 02092812-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kuroiwa,Y., Tomizuka,K., Yoshida,H. and Ishida,I.
  TITLE     Human artificial chromosomes comprising human antibody light chain
            lambda gene, and non-human animals retaining human artificial
            chromosome transmittable to progeny
  JOURNAL   Patent: WO 02092812-A 1 21-NOV-2002;
            KIRIN BREWERY CO LTD,YOSHIMI KUROIWA,KAZUMA TOMIZUKA, HITOSHI
            YOSHIDA, ISAO ISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 02092812-A/1
            PD   21-NOV-2002
            PF   10-MAY-2002 WO 2002JP004587
            PR   11-MAY-2001 JP 01P   142371
            PI   YOSHIMI KUROIWA,KAZUMA TOMIZUKA,HITOSHI YOSHIDA,ISAO ISHIDA PC
              C12N15/09,A01K67/027,C07K16/00,C12P21/08
            CC   Description of Artificial Sequence:primer
            FH   Key             Location/Qualifiers
            FT   source          1. .40
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT        5 a     14 c      6 g     15 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 30


RESULT 64
I12092
LOCUS       I12092                  42 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 33 from patent US 5420027.
ACCESSION   I12092
VERSION     I12092.1  GI:909590
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Fisher,C.W., Barnes,H.J. and Estabrook,R.W.
  TITLE     Methods and compositions for the expression of biologically active
            fusion proteins comprising a eukaryotic cytochrome P450 fused to a
            reductase in bacteria
  JOURNAL   Patent: US 5420027-A 33 30-MAY-1995;
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="unknown"
BASE COUNT        5 a      9 c      7 g     21 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 34
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RESULT 65
AX484623
LOCUS       AX484623                  43 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 1923 from Patent WO02053728.
ACCESSION   AX484623
VERSION     AX484623.1  GI:22318975
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 1923 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Candida albicans"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5476"
BASE COUNT        7 a      5 c      2 g     29 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 21


RESULT 66
AX061875/c
LOCUS       AX061875                  45 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 8 from Patent WO0078978.
ACCESSION   AX061875
VERSION     AX061875.1  GI:12539921
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Miller,B.G., Sloan,J.S., Raymond,C.K. and Vanaja,E.
  TITLE     Pichia methanolica glyceraldehyde-3-phosphate dehydrogenase 1
            promoter and terminator
  JOURNAL   Patent: WO 0078978-A 8 28-DEC-2000;
            ZymoGenetics, Inc. (US) ; Miller, Brady G. (US) ; Sloan, James S.
            (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC12,565"
BASE COUNT       23 a      9 c      8 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 67
ATH528602/c
LOCUS       ATH528602                 45 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            168E06.
ACCESSION   AJ528602
VERSION     AJ528602.1  GI:26796862
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 45)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="168E06"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .45
                     /note="T-DNA flanking sequence
                     left border"
BASE COUNT       16 a      8 c      9 g     12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 8;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 68
AR284713
LOCUS       AR284713                  47 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 765 from patent US 6528260.
ACCESSION   AR284713
VERSION     AR284713.1  GI:29721617
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Blumenfeld,M., Chumakov,I., Bougueleret,L. and Cohen,A.
  TITLE     Biallelic markers related to genes involved in drug metabolism
  JOURNAL   Patent: US 6528260-A 765 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
```

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BASE COUNT        6 a     11 c      8 g     21 t      1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          1 CTTCTCTTTT 10


RESULT 69
AR288787/c
LOCUS       AR288787                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 522 from patent US 6537751.
ACCESSION   AR288787
VERSION     AR288787.1  GI:31676071
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 522 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       16 a      4 c     18 g      8 t      1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 70
AR289547
LOCUS       AR289547                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1282 from patent US 6537751.
ACCESSION   AR289547
VERSION     AR289547.1  GI:31676831
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 1282 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT        9 a     12 c     10 g     15 t      1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 22


RESULT 71
AR289811
LOCUS       AR289811                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1546 from patent US 6537751.
ACCESSION   AR289811
VERSION     AR289811.1  GI:31677095
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 1546 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT        5 a     14 c      2 g     24 t      2 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          9 CTTCTCTTTT 18


RESULT 72
AR290737/c
LOCUS       AR290737                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2472 from patent US 6537751.
ACCESSION   AR290737
VERSION     AR290737.1  GI:31678021
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 2472 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       24 a      6 c      7 g      9 t      1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         45 CTTCTCTTTT 36


RESULT 73
AR291549/c
LOCUS       AR291549                  47 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3284 from patent US 6537751.
ACCESSION   AR291549
VERSION     AR291549.1  GI:31678833
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
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  JOURNAL   Patent: US 6537751-A 3284 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="unknown"
BASE COUNT       19 a      4 c     12 g     11 t      1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         41 CTTCTCTTTT 32


RESULT 74
AR139658/c
LOCUS       AR139658                  50 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 37 from patent US 6207389.
ACCESSION   AR139658
VERSION     AR139658.1  GI:14482154
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Dosch,H.Michael.
  TITLE     Methods of controlling T lymphocyte mediated immune responses
  JOURNAL   Patent: US 6207389-A 37 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT       20 a      8 c     16 g      6 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         42 CTTCTCTTTT 33


RESULT 75
AX158156
LOCUS       AX158156                  50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1484 from Patent WO0140521.
ACCESSION   AX158156
VERSION     AX158156.1  GI:14539487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 1484 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg29689883"
     misc_feature    26
                     /note="2 of 2 allelic variants (1483 is other entry)"
BASE COUNT        4 a      9 c      2 g     35 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         26 CTTCTCTTTT 35


RESULT 76
AX118141
LOCUS       AX118141                  51 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 3264 from Patent WO0129262.
ACCESSION   AX118141
VERSION     AX118141.1  GI:14035092
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 3264 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        8 a      13 c      3 g     27 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 20


RESULT 77
AX158155
LOCUS       AX158155                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1483 from Patent WO0140521.
ACCESSION   AX158155
VERSION     AX158155.1  GI:14539486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 1483 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (1484 is other entry)
                     Accession number cg29689883"
BASE COUNT        4 a      9 c      2 g     36 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 51;
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  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         27 CTTCTCTTTT 36


RESULT 78
AX160381
LOCUS       AX160381                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3709 from Patent WO0140521.
ACCESSION   AX160381
VERSION     AX160381.1  GI:14541712
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 3709 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (3710 is other entry)
                     Accession number cg43917418"
BASE COUNT        7 a     15 c     10 g     19 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         40 CTTCTCTTTT 49


RESULT 79
AX160382
LOCUS       AX160382                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3710 from Patent WO0140521.
ACCESSION   AX160382
VERSION     AX160382.1  GI:14541713
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 3710 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="2 of 2 allelic variants (3709 is other entry)
                     Accession number cg43917418"
BASE COUNT        7 a     16 c     10 g     18 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         40 CTTCTCTTTT 49


RESULT 80
AX160383
LOCUS       AX160383                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3711 from Patent WO0140521.
ACCESSION   AX160383
VERSION     AX160383.1  GI:14541714
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 3711 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (3712 is other entry)
                     Accession number cg43917418"
BASE COUNT        6 a     12 c     10 g     23 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 34


RESULT 81
AX165562
LOCUS       AX165562                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 757 from Patent WO0138586.
ACCESSION   AX165562
VERSION     AX165562.1  GI:14546391
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0138586-A 757 31-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg43917191"
BASE COUNT       12 a     12 c      7 g     20 t
ORIGIN
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  Query Match             100.0%;  Score 10;  DB 6;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          2 CTTCTCTTTT 11


RESULT 82
ATH521150
LOCUS       ATH521150                 51 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            260A09.
ACCESSION   AJ521150
VERSION     AJ521150.1  GI:26789386
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 51)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="260A09"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .51
                     /note="T-DNA flanking sequence
                     left border"
BASE COUNT       15 a      9 c      2 g     25 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 8;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          4 CTTCTCTTTT 13


RESULT 83
AR098682/c
LOCUS       AR098682                  53 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 40 from patent US 6077668.
ACCESSION   AR098682
VERSION     AR098682.1  GI:12808448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 40 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT       20 a      10 c      15 g       8 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 84
AR098683
LOCUS       AR098683                  53 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 41 from patent US 6077668.
ACCESSION   AR098683
VERSION     AR098683.1  GI:12808449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 41 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT        8 a      15 c      10 g      20 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 47


RESULT 85
AR204756/c
LOCUS       AR204756                  53 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 40 from patent US 6368802.
ACCESSION   AR204756
VERSION     AR204756.1  GI:21502164
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 40 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
```

```
BASE COUNT       20 a     10 c     15 g      8 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 86
AR204757
LOCUS       AR204757                  53 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 41 from patent US 6368802.
ACCESSION   AR204757
VERSION     AR204757.1  GI:21502165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 41 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT        8 a     15 c     10 g     20 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 47


RESULT 87
AR134108/c
LOCUS       AR134108                  54 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2533 from patent US 6194150.
ACCESSION   AR134108
VERSION     AR134108.1  GI:14123013
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 2533 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="unknown"
BASE COUNT       20 a     12 c     13 g      9 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 88
AR134285/c
LOCUS       AR134285                  54 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2710 from patent US 6194150.
ACCESSION   AR134285
VERSION     AR134285.1  GI:14123190
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 2710 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="unknown"
BASE COUNT       21 a     11 c     12 g     10 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 89
ATH505724
LOCUS       ATH505724                 57 bp    mRNA    linear   PLN 30-APR-2003
DEFINITION  Arabidopsis thaliana partial mitochondrial small non-messenger RNA,
            clone Ath-647, 5' end incomplete.
ACCESSION   AJ505724
VERSION     AJ505724.1  GI:22293620
KEYWORDS    small non-messenger RNA; snmRNA.
SOURCE      mitochondrion Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Marker,C., Zemann,A., Terhorst,T., Kiefmann,M., Kastenmayer,J.P.,
            Green,P., Bachellerie,J.P., Brosius,J. and Huttenhofer,A.
  TITLE     Experimental RNomics. Identification of 140 Candidates for Small
            Non-Messenger RNAs in the Plant Arabidopsis thaliana
  JOURNAL   Curr. Biol. 12 (23), 2002-2013 (2002)
  MEDLINE   22365595
   PUBMED   12477388
REFERENCE   2  (bases 1 to 57)
  AUTHORS   Huttenhofer,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUL-2002) Huttenhofer A., University of Muenster,
            Institute for Experimental Pathology, Von-Esmarch-Str. 56, 48149
            Muenster, GERMANY
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Arabidopsis thaliana"
                     /organelle="mitochondrion"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="Ath-647"
     misc_RNA        <1. .57
                     /note="small non-messenger RNA, snmRNA"
BASE COUNT        6 a     10 c      8 g     33 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 8;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         45 CTTCTCTTTT 54
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RESULT 90
ATH527067/c
LOCUS       ATH527067                58 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            131H07.
ACCESSION   AJ527067
VERSION     AJ527067.1  GI:26795327
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 58)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="131H07"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .58
                     /note="T-DNA flanking sequence
                     left border"
BASE COUNT       18 a      4 c     14 g     22 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 8;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         47 CTTCTCTTTT 38


RESULT 91
AX270701
LOCUS       AX270701                 61 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1332 from Patent WO0164876.
ACCESSION   AX270701
VERSION     AX270701.1  GI:16543477
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Stefansson,H., Steinthorsdottir,V. and Gulcher,J.R.
  TITLE     Human schizophrenia gene
  JOURNAL   Patent: WO 0164876-A 1332 07-SEP-2001;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1. .61
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      23 c       0 g      35 t       1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26


RESULT 92
AX272232
LOCUS       AX272232                 61 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1332 from Patent WO0164877.
ACCESSION   AX272232
VERSION     AX272232.1  GI:16544969
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Stefansson,H., Steinthorsdottir,V. and Gulcher,J.R.
  TITLE     Human schizophrenia gene
  JOURNAL   Patent: WO 0164877-A 1332 07-SEP-2001;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1. .61
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT        2 a      23 c       0 g      35 t       1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26


RESULT 93
AX482835
LOCUS       AX482835                 65 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 135 from Patent WO02053728.
ACCESSION   AX482835
VERSION     AX482835.1  GI:22317255
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 135 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .65
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                /organism="Candida albicans"
                /mol_type="genomic DNA"
                /db_xref="taxon:5476"
BASE COUNT        5 a      22 c       2 g      36 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          2 CTTCTCTTTT 11


RESULT 94
AX482852
LOCUS       AX482852                 65 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 152 from Patent WO02053728.
ACCESSION   AX482852
VERSION     AX482852.1  GI:22317272
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 152 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Candida albicans"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5476"
BASE COUNT       17 a     16 c      5 g     27 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 24


RESULT 95
AX485490
LOCUS       AX485490                 65 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 2790 from Patent WO02053728.
ACCESSION   AX485490
VERSION     AX485490.1  GI:22319774
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 2790 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Candida albicans"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5476"
BASE COUNT       15 a      6 c      6 g     38 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 34


RESULT 96
A81696
LOCUS       A81696                   70 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 1 from Patent WO9900504.
ACCESSION   A81696
VERSION     A81696.1  GI:6731831
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Sleep,D.
  TITLE     IMPROVED PROTEIN EXPRESSION STRAINS
  JOURNAL   Patent: WO 9900504-A 1 07-JAN-1999;
            DELTA BIOTECHNOLOGY LTD (GB); SLEEP DARRELL (GB)
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT       15 a     17 c      6 g     32 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         30 CTTCTCTTTT 39


RESULT 97
AR207788
LOCUS       AR207788                 70 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from patent US 6379924.
ACCESSION   AR207788
VERSION     AR207788.1  GI:21507632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Sleep,D.
  TITLE     Protein expression strains
  JOURNAL   Patent: US 6379924-A 1 30-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="unknown"
BASE COUNT       15 a     17 c      6 g     32 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         30 CTTCTCTTTT 39


RESULT 98
I62432
LOCUS       I62432                   71 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 5 from patent US 5659122.
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ACCESSION   I62432
VERSION     I62432.1  GI:2480380
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Austin,G.Douglas.
  TITLE     Enhanced expression in plants using non-translated leader sequences
  JOURNAL   Patent: US 5659122-A 5 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="unknown"
BASE COUNT       28 a     17 c      5 g     21 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 99
AH006998S06
LOCUS       AH006998S06               71 bp    DNA     linear   PRI 27-SEP-2002
DEFINITION  Homo sapiens mitochondrial short-chain L-3-hydroxyacyl-CoA
            dehydrogenase (HADHSC) gene, nuclear gene encoding mitochondrial
            protein, 5' end of intron 3.
ACCESSION   AF026858
VERSION     AF026858.1  GI:3882441
KEYWORDS    .
SEGMENT     6 of 15
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Vredendaal,P.J., van den Berg,I.E., Stroobants,A.K., van der
            A,D.L., Malingre,H.E. and Berger,R.
  TITLE     Structural organization of the human short-chain
            L-3-hydroxyacyl-CoA dehydrogenase gene
  JOURNAL   Mamm. Genome 9 (9), 763-768 (1998)
  MEDLINE   98384544
   PUBMED   9716664
REFERENCE   2  (bases 1 to 71)
  AUTHORS   Vredendaal,P.J.C.M., van den Berg,I.E.T., Stroobants,A.K., van der
            A,D.L., Malingre,H.E.M. and Berger,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-SEP-1997) Department of Metabolic Diseases,
            Wilhelmina Children's Hospital, Nieuwe Gracht 137, Utrecht 3512 LK,
            The Netherlands
FEATURES             Location/Qualifiers
     source          1. .71
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                     /chromosome="4"
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     intron          1. .>71
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ORIGIN

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Qy          1 CTTCTCTTTT 10
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Db         21 CTTCTCTTTT 30


RESULT 100
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LOCUS       BD055583                  73 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sequence tag and encoded human protein.
ACCESSION   BD055583
VERSION     BD055583.1  GI:22601189
KEYWORDS    JP 2001269182-A/31829.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
  TITLE     Sequence tag and encoded human protein
  JOURNAL   Patent: JP 2001269182-A 31829 02-OCT-2001;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001269182-A/31829
            PD   02-OCT-2001
            PF   24-FEB-2000 JP 2000118773
            PR   26-FEB-1999 US    60/122487
            PI   JEAN BAPUTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI   JORDAN
            PC   C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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BASE COUNT       19 a     10 c      17 g     27 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 73;
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Db         29 CTTCTCTTTT 20


Search completed: October 28, 2003, 17:43:55
Job time : 1553 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 28, 2003, 15:10:20 ; Search time 272 Seconds
(without alignments)
99.244 Million cell updates/sec

Title: US-09-335-032-71
Perfect score: 10
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	10	100.0	10	22	AAF34233	Yeast NORF gene SA
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	7	10	100.0	12	20	AAX14859	Triple helix third
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	33	10	100.0	20	18	AAT76779	Staphylococcus aur
	34	10	100.0	20	20	AAZ04007	PCR primer used to
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c	36	10	100.0	20	25	AAL51617	Human interferon a
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c	38	10	100.0	21	20	AAV08126	Primer Vbeta14 for
c	39	10	100.0	21	21	AAA95613	TCR Vbeta 14 subfa
c	40	10	100.0	21	22	AAH27157	Downstream PCR pri
c	41	10	100.0	21	23	AAS95067	Human otoferlin ex
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c	52	10	100.0	24	20	AAX88135	T cell receptor be
c	53	10	100.0	24	22	AAI99892	Human dihydroorota
c	54	10	100.0	24	22	AAH19640	Melon fusarium wil
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c	57	10	100.0	24	24	ABA04339	Human BolA structu
c	58	10	100.0	24	24	ABL45589	Human chromosome 2
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c 92	10	100.0	27	15	AAQ45398	Oligonucleotide fo
c 93	10	100.0	27	18	AAX74299	Mouse flt-1 VEGF r
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c 95	10	100.0	27	22	AAH38166	SNP specific lower
96	10	100.0	28	22	AAC81508	Human MSF exon 6 R
c 97	10	100.0	29	21	AAF05757	Hammerhead ribozym
98	10	100.0	29	21	AAA40663	Human CD36 polymor
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100	10	100.0	30	21	AAA40664	Human CD36 polymor
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103	10	100.0	31	20	AAX38879	Human genomic DNA
c 104	10	100.0	31	25	ABZ22465	Human MTSP10 PCR p
c 105	10	100.0	32	16	AAT07410	Primer Vbeta14/Eco
c 106	10	100.0	33	19	AAV39876	Streptococcus pneu
107	10	100.0	33	20	AAX35508	PCR primer used to
c 108	10	100.0	33	24	ABQ85037	Streptococcus pneu
c 109	10	100.0	36	25	ABZ22462	Human MTSP10 PCR p
c 110	10	100.0	38	23	ABK03875	Human NOGO Hammerh
111	10	100.0	38	23	ABK05785	Human NOGO Zinzyme
112	10	100.0	40	14	AAQ40864	VAC-beta gene prim
113	10	100.0	40	21	AAA96817	Forward PCR primer
114	10	100.0	40	25	ABZ70085	Human chromosome 2
c 115	10	100.0	41	24	ABK90429	Human shearing fac
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117	10	100.0	42	13	AAQ27383	Bovine 17-alpha-hy
118	10	100.0	42	15	AAQ55121	Human liver P450 2
c 119	10	100.0	42	20	AAX89210	Primer for constru
c 120	10	100.0	42	22	AAH84248	Human cell death p
121	10	100.0	43	24	ABZ27976	Candida essential
c 122	10	100.0	45	22	AAD02419	Pichia methanolica
123	10	100.0	47	20	AAX03631	Actinia equina L.
c 124	10	100.0	47	21	AAZ66175	Human map-related
125	10	100.0	47	21	AAZ66935	Human map-related
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c 129	10	100.0	48	22	AAH84247	Human cell death p
c 130	10	100.0	50	21	AAA77160	Human clone cg4394
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c 132	10	100.0	50	22	AAS03094	Mouse brain p69 5'
133	10	100.0	50	24	ABZ02704	Human leukocyte ge
134	10	100.0	50	24	ABZ04201	Human leukocyte ge
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136	10	100.0	50	24	ABZ06159	Human leukocyte ge
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c 138	10	100.0	51	21	AAA77161	Human clone cg4394
139	10	100.0	51	22	AAL27570	Human SNP oligonuc
c 140	10	100.0	51	22	AAL30883	Human SNP oligonuc
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144	10	100.0	51	22	AAI76768	Human silent SNP c
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150	10	100.0	53	19	AAV59246	Stem loop RNA mult
c 151	10	100.0	53	19	AAV12931	Oligonucleotide SE
152	10	100.0	53	19	AAV12932	Oligonucleotide SE
153	10	100.0	53	20	AAX30035	RNA oligonucleotid
c 154	10	100.0	54	17	AAX67061	Mouse B7 hairpin r
c 155	10	100.0	54	17	AAX67237	Mouse CD40 hairpin
c 156	10	100.0	60	10	AAN91187	Alpha-factor leade
157	10	100.0	60	24	ABN45634	Human spliced tran
c 158	10	100.0	60	24	ABN59213	Human spliced tran
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160	10	100.0	61	22	AAK98026	Human neuregulin g
161	10	100.0	61	24	ABT01303	Human neuregulin-1
162	10	100.0	61	24	ABT02796	Human neuregulin-1
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164	10	100.0	63	25	ABX55167	Bovine EST associa
165	10	100.0	65	24	ABZ26256	Candida essential
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167	10	100.0	65	24	ABZ28775	Candida gene relat
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173	10	100.0	70	20	AAV99879	S. cerevisiae UBC4
174	10	100.0	71	15	AAQ78295	Heat shock protein
175	10	100.0	71	16	AAQ81861	Sense strand of th
176	10	100.0	71	21	AAZ46993	Soybean HSP17.9 le
c 177	10	100.0	73	21	AAC31838	Human secreted pro
c 178	10	100.0	75	16	AAQ81862	Antisense strand o
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180	10	100.0	76	21	AAC15151	Human secreted pro
181	10	100.0	76	24	ABN83918	Soybean GmHSP17.9
182	10	100.0	78	15	AAQ78302	Heat shock protein
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184	10	100.0	83	21	AAC13898	Human secreted pro
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186	10	100.0	86	22	AAS23462	C. albicans essent
c 187	10	100.0	87	22	AAK23769	Human brain expres
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c 190	10	100.0	87	22	AAI55783	Probe #24469 used
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204	10	100.0	93	25	ABZ09458	Human oligonucleot
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207	10	100.0	97	16	AAT19418	Human gene signatu
c 208	10	100.0	97	22	ABA75204	Human foetal liver
c 209	10	100.0	97	22	ABA39867	Probe #18333 for g
c 210	10	100.0	97	22	AAK23739	Human brain expres
c 211	10	100.0	97	22	AAK49838	Human bone marrow
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c 219	10	100.0	102	22	ABA75552	Human foetal liver
c 220	10	100.0	102	22	ABA40165	Probe #18631 for g
c 221	10	100.0	102	22	AAK24128	Human brain expres
c 222	10	100.0	102	22	AAK50186	Human bone marrow
223	10	100.0	102	22	AAK89332	Human digestive sy
c 224	10	100.0	102	22	AAI27265	Probe #17198 for g
c 225	10	100.0	102	22	AAI56125	Probe #24811 used
c 226	10	100.0	102	23	ABS49816	Human liver single
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231	10	100.0	105	22	AAF83563	B. gymnorrhiza sal
c 232	10	100.0	105	24	ABL78374	Human ovarian canc
233	10	100.0	108	25	ABX55439	Bovine EST associa
234	10	100.0	112	17	AAT39029	PCR primer 593 for
235	10	100.0	114	22	ABA73004	Human foetal liver
236	10	100.0	114	22	ABA74146	Human foetal liver
237	10	100.0	114	22	ABA39160	Probe #17626 for g
238	10	100.0	114	22	AAK21436	Human brain expres
239	10	100.0	114	22	AAK22600	Human brain expres
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241	10	100.0	114	22	AAK48768	Human bone marrow
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247	10	100.0	114	24	ABS22480	Human genome-deriv
c 248	10	100.0	116	16	AAT22045	Human gene signatu
c 249	10	100.0	117	22	AAH84245	Human cell death p
250	10	100.0	118	22	ABA18306	Human nervous syst
c 251	10	100.0	118	24	ABT03406	Ovary cell-specifi
252	10	100.0	119	25	ABX30673	Human GDP-mannose
253	10	100.0	121	22	ABA77351	p53 mutation corre
c 254	10	100.0	121	22	ABA77352	p53 mutation corre
255	10	100.0	121	22	ABA77367	p53 mutation corre
c 256	10	100.0	121	22	ABA77368	p53 mutation corre
257	10	100.0	121	22	ABA77471	p53 mutation corre
c 258	10	100.0	121	22	ABA77472	p53 mutation corre
259	10	100.0	121	22	ABA77475	p53 mutation corre
c 260	10	100.0	121	22	ABA77476	p53 mutation corre
261	10	100.0	123	22	AAL03420	Human reproductive
262	10	100.0	123	22	AAL03421	Human reproductive
263	10	100.0	124	21	AAA41960	Human secreted exp
c 264	10	100.0	125	16	AAT05584	Mouse brain p69 cD
265	10	100.0	125	21	AAC09800	Human secreted pro
266	10	100.0	125	24	ABS72812	Human gene trapped
c 267	10	100.0	125	24	ABL70682	Corn tassel-derive
268	10	100.0	126	20	AAX82264	Modified intron (I
c 269	10	100.0	126	22	AAH84244	Human cell death p
c 270	10	100.0	128	21	AAA26486	Human prostate can
271	10	100.0	129	22	AAK24208	Human brain expres
272	10	100.0	129	22	AAI56202	Probe #24888 used
273	10	100.0	129	23	ABS49882	Human liver single
274	10	100.0	129	24	ABS23722	Human genome-deriv
c 275	10	100.0	132	20	AAX55702	DNA sequence encod
276	10	100.0	132	22	ABA70763	Human foetal liver
277	10	100.0	132	22	ABA37258	Probe #15724 for g
278	10	100.0	132	22	AAK19016	Human brain expres
279	10	100.0	132	22	AAK44967	Human bone marrow
280	10	100.0	132	22	AAI25083	Probe #15016 for g
281	10	100.0	132	22	AAI50936	Probe #19622 used
282	10	100.0	132	23	ABS44633	Human liver single
283	10	100.0	132	24	ABS19212	Human genome-deriv
c 284	10	100.0	132	24	AAD24911	Eukaryote calpain
c 285	10	100.0	136	22	AAS04717	Gene expression pr
c 286	10	100.0	137	18	AAT42753	Chicken CHD-W clon
287	10	100.0	138	20	AAV89017	EST clone IK11. H
c 288	10	100.0	138	21	AAA69140	Bacteriophage 192
289	10	100.0	138	21	AAC25141	Human secreted pro
c 290	10	100.0	140	22	ABA72103	Human foetal liver
c 291	10	100.0	140	22	ABA38038	Probe #16504 for g
c 292	10	100.0	140	22	AAK20530	Human brain expres
c 293	10	100.0	140	22	AAK46670	Human bone marrow
c 294	10	100.0	140	22	AAI25699	Probe #15632 for g
c 295	10	100.0	140	22	AAI52506	Probe #21192 used
c 296	10	100.0	140	23	ABS46445	Human liver single
c 297	10	100.0	140	24	ABS21024	Human genome-deriv
298	10	100.0	141	21	AAC32152	Human secreted pro
c 299	10	100.0	142	21	AAF10097	Fusarium venenatum
300	10	100.0	146	22	ABA71048	Human foetal liver
301	10	100.0	146	22	AAK19330	Human brain expres
302	10	100.0	146	22	AAK45307	Human bone marrow
303	10	100.0	146	22	AAI51261	Probe #19947 used
c 304	10	100.0	146	22	AAS03093	Mouse brain p69 5'
305	10	100.0	146	23	ABS44986	Human liver single
306	10	100.0	146	24	ABS19564	Human genome-deriv
c 307	10	100.0	147	21	AAC23129	Human secreted pro
c 308	10	100.0	147	22	AAS34332	Human cDNA encodin
309	10	100.0	147	24	ABK85007	DNA encoding cadhe
c 310	10	100.0	147	24	ABK29624	Colon adenocarcino
311	10	100.0	148	21	AAC19931	Human secreted pro
312	10	100.0	148	21	AAC20151	Human secreted pro
c 313	10	100.0	149	22	AAI68590	S. tuberosum SUT1
314	10	100.0	150	19	AAX10878	Human biallelic po
315	10	100.0	150	19	AAX10879	Human biallelic po
c 316	10	100.0	150	19	AAX12142	Human biallelic po
317	10	100.0	150	19	AAX10503	Human biallelic po
318	10	100.0	150	19	AAX10504	Human biallelic po
319	10	100.0	152	21	AAC04835	Human secreted pro
c 320	10	100.0	155	21	AAA43003	Human secreted exp
c 321	10	100.0	156	22	AAH84243	Human cell death p
c 322	10	100.0	156	24	ABK76880	Bacillus lichenifo
323	10	100.0	156	24	ABN70111	Streptococcus poly
c 324	10	100.0	156	24	ABN70111	Streptococcus poly
325	10	100.0	157	22	AAI61613	Soybean 318013 reg
326	10	100.0	159	21	AAF09897	Fusarium venenatum
327	10	100.0	159	21	AAC05820	Human secreted pro
328	10	100.0	161	22	AAK74123	Human immune/haema
329	10	100.0	161	22	AAK74124	Human immune/haema
330	10	100.0	161	22	AAK74125	Human immune/haema
331	10	100.0	161	22	AAF66665	Novel human polynu
332	10	100.0	162	21	AAC22120	Human secreted pro
c 333	10	100.0	163	24	ABV96596	Human pancreatic c
c 334	10	100.0	163	25	ABZ78829	Tumour suppression
c 335	10	100.0	163	25	ABZ09376	Human oligonucleot
336	10	100.0	164	16	AAT26273	Human gene signatu
337	10	100.0	164	16	AAT21185	Human gene signatu
338	10	100.0	169	15	AAQ76860	Human genome fragm
339	10	100.0	169	22	AAS24514	Human ovarian PCR-
340	10	100.0	169	25	ABX65068	Human gene trapped
341	10	100.0	170	22	AAH83122	Human ovarian tumo
c 342	10	100.0	172	21	AAC26682	Human secreted pro
343	10	100.0	173	21	AAA42237	Human secreted exp
c 344	10	100.0	174	22	AAK23967	Human brain expres
c 345	10	100.0	174	22	AAI55976	Probe #24662 used
c 346	10	100.0	174	22	AAH84242	Human cell death p
c 347	10	100.0	176	21	AAC27878	Human secreted pro
c 348	10	100.0	177	22	AAK58944	Human immune/haema
c 349	10	100.0	178	22	AAK72814	Human immune/haema
350	10	100.0	178	23	ABK41929	cDNA encoding nove
c 351	10	100.0	180	24	ABN70012	Streptococcus poly
352	10	100.0	181	22	AAI61656	Soybean 318013 reg
353	10	100.0	182	24	ABL63623	Breast cancer rela
354	10	100.0	183	22	ABA70927	Human foetal liver
355	10	100.0	183	22	ABA37362	Probe #15828 for g
356	10	100.0	183	22	AAK19197	Human brain expres
357	10	100.0	183	22	AAK45162	Human bone marrow
358	10	100.0	183	22	AAI25164	Probe #15097 for g
359	10	100.0	183	22	AAI51115	Probe #19801 used
360	10	100.0	183	23	ABS44834	Human liver single
361	10	100.0	183	24	ABS19412	Human genome-deriv
c 362	10	100.0	184	22	AAH23118	Osteoarthritis tis
c 363	10	100.0	186	22	AAK47486	*Human bone marrow*
364	10	100.0	186	22	AAD17126	Human ion channel-
c 365	10	100.0	186	23	ABS47223	Human liver single
c 366	10	100.0	186	25	ABZ40589	N. gonorrhoeae nuc
c 367	10	100.0	187	21	AAC19483	Human secreted pro
368	10	100.0	189	21	AAA69122	Bacteriophage 192
c 369	10	100.0	189	21	AAC16524	Human secreted pro
c 370	10	100.0	189	22	AAH84241	Human cell death p
371	10	100.0	190	21	AAC72727	Single nucleotide
372	10	100.0	190	21	AAC72757	Single nucleotide
373	10	100.0	191	21	AAC04705	Human secreted pro

c	374	10	100.0	192	21	AAC46510	Arabidopsis thalia
	375	10	100.0	192	22	ABA74930	Human foetal liver
	376	10	100.0	192	22	ABA39620	Probe #18086 for g
	377	10	100.0	192	22	AAK23426	Human brain expres
	378	10	100.0	192	22	AAK49575	Human bone marrow
	379	10	100.0	192	22	AAI26683	Probe #16616 for g
	380	10	100.0	192	22	AAI55455	Probe #24141 used
	381	10	100.0	192	23	ABS49199	Human liver single
	382	10	100.0	192	24	ABS23061	Human genome-deriv
	383	10	100.0	192	25	ABX24071	Human GDP-mannose
c	384	10	100.0	193	22	AAC89225	Human brain T calc
c	385	10	100.0	194	21	AAC23146	Human secreted pro
	386	10	100.0	194	22	AAK85847	Human immune/haema
c	387	10	100.0	194	24	ABT05943	Human prostate spe
	388	10	100.0	195	21	AAC26414	Human secreted pro
c	389	10	100.0	195	22	AAH84240	Human cell death p
	390	10	100.0	197	22	AAH71352	Human cervical can
c	391	10	100.0	198	22	AAH23139	Osteoarthritis tis
	392	10	100.0	198	24	ABN77071	Human ORF2018 cDNA
c	393	10	100.0	198	25	ABZ39502	N. gonorrhoeae nuc
c	394	10	100.0	198	25	ABZ40923	N. gonorrhoeae nuc
	395	10	100.0	199	21	AAC07052	Human secreted pro
	396	10	100.0	200	19	AAX10761	Human biallelic po
	397	10	100.0	201	21	AAC17019	Human secreted pro
c	398	10	100.0	201	22	ABA89313	Escherichia coli p
	399	10	100.0	201	22	AAS08348	Human CLASP-4 Geno
c	400	10	100.0	201	24	ABK76931	Bacillus lichenifo
	401	10	100.0	201	24	ABN17225	Human ORFX polynuc
c	402	10	100.0	201	25	ABX27535	Human GDP-mannose
c	403	10	100.0	202	23	ABV08734	Human prostate exp
c	404	10	100.0	202	25	ABX94314	Human breast speci
	405	10	100.0	203	23	AAS50177	Staphylococcus aur
	406	10	100.0	204	21	AAC19011	Human secreted pro
c	407	10	100.0	204	21	AAA26487	Human prostate can
	408	10	100.0	204	22	ABA47082	Human breast cell
	409	10	100.0	204	22	ABA64966	Human foetal liver
	410	10	100.0	204	22	ABA32074	Probe #10540 for g
	411	10	100.0	204	22	AAI19938	Probe #9871 for ge
	412	10	100.0	204	22	AAI45134	Probe #13820 used
	413	10	100.0	204	22	AAI05651	Probe #5642 used t
	414	10	100.0	204	23	ABS38714	Human liver single
	415	10	100.0	204	24	ABS13212	Human genome-deriv
c	416	10	100.0	205	22	AAK77269	Human immune/haema
c	417	10	100.0	205	24	ABN62589	Human cancer relat
	418	10	100.0	206	22	AAK60253	Human immune/haema
	419	10	100.0	206	25	ABX88544	Corn ear-derived p
	420	10	100.0	206	25	ABX55898	Bovine EST associa
c	421	10	100.0	208	21	AAA31871	Plant microsatelli
	422	10	100.0	208	24	ABN76923	Human ORF1870 cDNA
	423	10	100.0	210	22	AAK18614	Human brain expres
	424	10	100.0	210	22	AAK44535	Human bone marrow
	425	10	100.0	210	22	AAI50523	Probe #19209 used
	426	10	100.0	210	23	ABS44193	Human liver single
c	427	10	100.0	210	24	AAD40072	Human DAP3 (DED co
c	428	10	100.0	210	24	ABQ69691	Listeria innocua D
	429	10	100.0	210	24	ABS18772	Human genome-deriv
	430	10	100.0	212	21	AAC21286	Human secreted pro
	431	10	100.0	212	24	ABQ81920	Kaposi's Sarcoma T
c	432	10	100.0	212	25	ABZ18650	Group III cDNA can
	433	10	100.0	213	21	AAC05128	Human secreted pro
c	434	10	100.0	213	21	AAC29873	Human secreted pro
c	435	10	100.0	213	22	AAH84239	Human cell death p
c	436	10	100.0	213	25	ABX31036	Human GDP-mannose
c	437	10	100.0	215	22	AAH84417	E. coli growth and
	438	10	100.0	216	21	AAC24889	Human secreted pro
c	439	10	100.0	217	21	AAC07070	Human secreted pro
	440	10	100.0	217	21	AAC32131	Human secreted pro
	441	10	100.0	218	21	AAC32318	Human secreted pro
c	442	10	100.0	218	22	ABA48671	Human breast cell
c	443	10	100.0	218	22	ABA66585	Human foetal liver
c	444	10	100.0	218	22	ABA33652	Probe #12118 for g
c	445	10	100.0	218	22	AAK15012	Human brain expres
c	446	10	100.0	218	22	AAK40743	Human bone marrow
c	447	10	100.0	218	22	AAI21506	Probe #11439 for g
c	448	10	100.0	218	22	AAI46798	Probe #15484 used
c	449	10	100.0	218	22	AAI07202	Probe #7193 used t
c	450	10	100.0	218	23	ABS40316	Human liver single
c	451	10	100.0	218	24	ABS14697	Human genome-deriv
	452	10	100.0	218	24	ABL87111	Human ovarian canc
	453	10	100.0	219	21	AAA44467	Human secreted exp
c	454	10	100.0	223	21	AAC08908	Human secreted pro
c	455	10	100.0	224	23	AAS75432	DNA encoding novel
c	456	10	100.0	224	24	AAD34641	HBV infection regu
	457	10	100.0	225	21	AAC09598	Human secreted pro
	458	10	100.0	226	20	AAV89452	EST clone CO444.
c	459	10	100.0	226	24	ABS72311	Human gene trapped
c	460	10	100.0	228	24	ABK78344	Bacillus clausii g
c	461	10	100.0	228	25	ACA55501	Human signalling p
	462	10	100.0	229	18	AAV78907	Staphylococcus aur
	463	10	100.0	231	22	ABA50939	Human breast cell
	464	10	100.0	231	22	ABA68918	Human foetal liver
	465	10	100.0	231	22	ABA35871	Probe #14337 for g
	466	10	100.0	231	22	AAK17250	Human brain expres
	467	10	100.0	231	22	AAK43039	Human bone marrow
	468	10	100.0	231	22	AAI23802	Probe #13735 for g
	469	10	100.0	231	22	AAI49114	Probe #17800 used
	470	10	100.0	231	22	AAI09411	Probe #9402 used t
	471	10	100.0	231	22	AAH69050	Human cervical can
c	472	10	100.0	231	22	AAH84238	Human cell death p
	473	10	100.0	231	23	ABS42674	Human liver single
	474	10	100.0	231	24	ABS17104	Human genome-deriv
c	475	10	100.0	232	23	ABV17269	Human prostate exp
	476	10	100.0	232	24	ABV96475	Human pancreatic c
c	477	10	100.0	233	20	AAX97615	Extended human sec
	478	10	100.0	233	22	ABA73832	Human foetal liver
	479	10	100.0	233	22	AAK22283	Human brain expres
	480	10	100.0	233	22	AAK48449	Human bone marrow
	481	10	100.0	233	22	AAI54276	Probe #22962 used
c	482	10	100.0	237	14	AAQ37074	T cell receptor be
	483	10	100.0	238	21	AAA43118	Human secreted exp
c	484	10	100.0	238	22	AAH29107	Drosophila melanog
c	485	10	100.0	239	20	AAV87545	EST clone DT306.
c	486	10	100.0	239	21	AAC05148	Human secreted pro
	487	10	100.0	239	21	AAC24560	Human secreted pro
c	488	10	100.0	240	14	AAQ37075	T cell receptor be
	489	10	100.0	240	20	AAV89137	EST clone BR312.
c	490	10	100.0	240	24	ABL71901	Corn tassel-derive
	491	10	100.0	241	22	AAS47302	Human breast cance
	492	10	100.0	241	22	AAF17872	Human breast cance
	493	10	100.0	241	24	ABS63903	Human breast tumou
	494	10	100.0	241	24	ABT06894	Human ovarian canc
	495	10	100.0	241	25	ABT33115	Human tumour-relat
	496	10	100.0	241	25	ABX72772	Human ovarian carc
c	497	10	100.0	243	21	AAA44176	Mouse secreted exp
c	498	10	100.0	243	22	AAF15377	Mycoplasma genital
	499	10	100.0	244	24	AAD42893	Maize sugary1 (SU1
	500	10	100.0	246	22	AAH69927	Human cervical can

ALIGNMENTS

RESULT 1
AAV50115
ID AAV50115 standard; DNA; 10 BP.
XX
AC AAV50115;
XX
DT 21-OCT-1998 (first entry)
XX
DE Yeast tag for NORF gene locus NORF5.
XX
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle;
KW regulation; eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX

OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9832847-A2.
XX
PD 30-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US01216.
XX
PR 23-JAN-1997; 97US-0035917.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Kinzler KW, Velculescu VE, Vogelstein B;
XX
DR WPI; 1998-427943/36.
XX
PT Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression
XX
PS Claim 1; Page 23; 44pp; English.
XX
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast
CC gene involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes
CC (SAGE tags given in AAV50051 to AAV50345); (2) a method for screening
CC candidate antifungal drugs which comprises contacting a test substance
CC with a yeast cell and monitoring expression of a yeast gene which is
CC involved in cell cycle progression; (3) a method of identifying human
CC genes which are involved in cell cycle progression which comprises
CC hybridizing a probe comprising at least 10 contiguous nucleotides of a
CC yeast gene which is differentially expressed between at least 2 phases
CC selected from the log phase, the S phase and the G2/M phase; and (4) a
CC probe for ascertaining the phase in the cell cycle, where the probe
CC comprises at least 14 contiguous nucleotides of a NORF gene (SAGE tags
CC given in AAV50051 to AAV50345), or as an array of probes on a solid
CC support.
XX
SQ Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 1 CTTCTCTTTT 10

RESULT 2
AAF33332
ID AAF33332 standard; DNA; 10 BP.
XX
AC AAF33332;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:71.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Claim 1; Page 23; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 1 CTTCTCTTTT 10

RESULT 3
AAF33921
ID AAF33921 standard; DNA; 10 BP.
XX
AC AAF33921;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:660.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Claim 1; Page 398; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 1 CTTCTCTTTT 10

RESULT 4
AAF33924
ID AAF33924 standard; DNA; 10 BP.
XX
AC AAF33924;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:663.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Claim 1; Page 398; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 1 CTTCTCTTTT 10

RESULT 5
AAF34233
ID AAF34233 standard; DNA; 10 BP.
XX
AC AAF34233;
XX

DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:972.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US16223.
XX
PR 16-JUN-1999; 99US-0335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
PS Example; Page 34; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
SQ Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 1 CTTCTCTTTT 10

RESULT 6
AAX14794/c
ID AAX14794 standard; DNA; 12 BP.
XX
AC AAX14794;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 807-818 of Hepatitis B virus.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-0173489.
XX
PR 22-DEC-1993; 93US-0173489.
PR 29-OCT-1992; 92US-0968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria
XX
PS Disclosure; Columns 19-20; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX
SQ Sequence 12 BP; 8 A; 0 C; 4 G; 0 U; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 11 CTTCTCTTTT 2

RESULT 7
AAX14859
ID AAX14859 standard; DNA; 12 BP.
XX
AC AAX14859;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix third strand of 23S rRNA gene nucleotides 214-225.
XX
KW Triplex formation; DNA detection; triple helix; identification;
KW bacteria; oncogene; virus; ss.
XX
OS Synthetic.

OS Micrococcus luteus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-0173489.
XX
PR 22-DEC-1993; 93US-0173489.
PR 29-OCT-1992; 92US-0968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria
XX
PS Disclosure; Columns 21-22; 168pp; English.
XX
CC The present sequence represents a polynucleotide that is able to
CC form a triple helix with a double stranded sequence. Cytosine bases
CC in the present can be replaced with 5-methylcytosine for increased
CC triplex stability. The present sequence is used in the assay of the
CC invention, where it can be part of the anchor DNA or reporter DNA
CC sequence. The assay comprises adding a sample containing double-stranded
CC DNA test sequences to an aqueous medium containing at least one complex
CC of anchor DNA, attached to a solid support, and reporter DNA, where
CC either a part of the anchor DNA or reporter DNA is designed to form
CC a triple-strand structure with part of the test sequence. Triplex
CC formation results in displacement of the reporter DNA which is
CC detected as an indication of the presence of the DNA test sequence.
CC The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX
SQ Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 3 CTTCTCTTTT 12

RESULT 8
ABH67817
ID ABH67817 standard; DNA; 12 BP.
XX
AC ABH67817;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 267794 for detecting SNP TSC0000531.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 267794; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 2 CTTCTCTTTT 11

RESULT 9
ABI80052
ID ABI80052 standard; DNA; 12 BP.
XX
AC ABI80052;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 380025 for detecting SNP TSC0063600.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 380025; 29pp + Sequence Listing; German.

XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 3 CTTCTCTTTT 12

RESULT 10
ABC07094/c
ID ABC07094 standard; DNA; 13 BP.
XX
AC ABC07094;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 7085 for detecting SNP TSC0002097.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 7085; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 13 CTTCTCTTTT 4

RESULT 11
ABC07095
ID ABC07095 standard; DNA; 13 BP.
XX
AC ABC07095;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 7086 for detecting SNP TSC0002097.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB00713.
XX
PR 07-APR-2000; 2000DE-1019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
PS Claim 1; SEQ ID 7086; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 1 CTTCTCTTTT 10

RESULT 12

```
ABC53772/c
ID   ABC53772 standard; DNA; 13 BP.
XX
AC   ABC53772;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 53789 for detecting SNP TSC0014813.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 53789; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 10 A; 0 C; 3 G; 0 U; 0 other;

  Query Match             100.0%;  Score 10;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 13
ABC53773
ID   ABC53773 standard; DNA; 13 BP.
XX
AC   ABC53773;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 53790 for detecting SNP TSC0014813.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 53790; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 0 A; 3 C; 0 G; 10 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          4 CTTCTCTTTT 13


RESULT 14
ABH25906/c
ID   ABH25906 standard; DNA; 13 BP.
XX
AC   ABH25906;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 225883 for detecting SNP TSC0055065.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
```

```
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 225883; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 8 A; 0 C; 3 G; 2 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 15
ABH25907
ID   ABH25907 standard; DNA; 13 BP.
XX
AC   ABH25907;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 225884 for detecting SNP TSC0055065.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB00713.
XX
PR   07-APR-2000; 2000DE-1019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single nucleotide polymorphisms and cytosine
PT   methylation status  -
XX
PS   Claim 1; SEQ ID 225884; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation.
CC   ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC   ABI00010-ABI82073 represent the oligomers described in the invention.
CC   NOTE: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 13 BP; 2 A; 3 C; 0 G; 8 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 23;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          4 CTTCTCTTTT 13


RESULT 16
ABV80474/c
ID   ABV80474 standard; DNA; 17 BP.
XX
AC   ABV80474;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1720.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 289; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
```

```
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 0 C; 7 G; 2 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 17
ABV80475/c
ID   ABV80475 standard; DNA; 17 BP.
XX
AC   ABV80475;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1721.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 289; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 18
ABV80476/c
ID   ABV80476 standard; DNA; 17 BP.
XX
AC   ABV80476;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1722.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 289; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
```

```
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 9 A; 0 C; 5 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 19
ABV80477/c
ID   ABV80477 standard; DNA; 17 BP.
XX
AC   ABV80477;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1723.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 289; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 20
ABV80478/c
ID   ABV80478 standard; DNA; 17 BP.
XX
AC   ABV80478;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1724.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 289; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
```

```
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 0 C; 6 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 21
ABV80479/c
ID   ABV80479 standard; DNA; 17 BP.
XX
AC   ABV80479;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1725.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 290; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 1 C; 5 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 22
ABV80480/c
ID   ABV80480 standard; DNA; 17 BP.
XX
AC   ABV80480;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1726.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
```

```
XX
PS   Example 2; Page 290; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 1 C; 4 G; 4 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 23
ABV80481/c
ID   ABV80481 standard; DNA; 17 BP.
XX
AC   ABV80481;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 1727.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-0001167.
XX
PR   30-JAN-2001; 2001WO-US00663.
PR   30-JAN-2001; 2001WO-US00664.
PR   30-JAN-2001; 2001WO-US00665.
PR   30-JAN-2001; 2001WO-US00667.
PR   30-JAN-2001; 2001WO-US00668.
PR   30-JAN-2001; 2001WO-US00669.
PR   23-MAY-2001; 2001US-0864761.
PR   09-OCT-2001; 2001US-0327898.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL),
PT   useful for identifying agonist and antagonist and specific binding
PT   partners, and for treating subjects having defects in HTPL -
XX
PS   Example 2; Page 290; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention.
XX
SQ   Sequence 17 BP; 8 A; 1 C; 5 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 24
ABS74761/c
ID   ABS74761 standard; DNA; 17 BP.
XX
AC   ABS74761;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 17-mer SEQ ID 287.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-0827998.
XX
PR   26-MAY-2000; 2000US-207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy  -
XX
PS   Example 2; Page 113; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes
```

CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 17 CTTCTCTTTT 8

RESULT 25
ABS74762/c
ID ABS74762 standard; DNA; 17 BP.
XX
AC ABS74762;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 288.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 16 CTTCTCTTTT 7

RESULT 26
ABS74763/c
ID ABS74763 standard; DNA; 17 BP.
XX
AC ABS74763;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 289.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 9 A; 2 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 15 CTTCTCTTTT 6

RESULT 27
ABS74764/c
ID ABS74764 standard; DNA; 17 BP.
XX
AC ABS74764;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 290.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 10 A; 1 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 14 CTTCTCTTTT 5

RESULT 28
ABS74765/c
ID ABS74765 standard; DNA; 17 BP.
XX
AC ABS74765;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 291.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 11 A; 1 C; 4 G; 1 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 13 CTTCTCTTTT 4

RESULT 29
ABS74766/c
ID ABS74766 standard; DNA; 17 BP.
XX
AC ABS74766;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 292.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX

PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 10 A; 1 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 12 CTTCTCTTTT 3

RESULT 30
ABS74767/c
ID ABS74767 standard; DNA; 17 BP.
XX
AC ABS74767;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 293.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 17 BP; 10 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 11 CTTCTCTTTT 2

RESULT 31
ABS74768/c
ID ABS74768 standard; DNA; 17 BP.
XX
AC ABS74768;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 294.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 113; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the

```
CC   human PAPP-E genes described in the disclosure of the invention.
XX
SQ   Sequence 17 BP; 9 A; 1 C; 4 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 32
ABX94543
ID   ABX94543 standard; DNA; 19 BP.
XX
AC   ABX94543;
XX
DT   13-JUN-2003  (first entry)
XX
DE   23S/16S rRNA detecting probe SEQ ID 12.
XX
KW   Detection; probe; contaminant; drinking water; Legionella; coliform;
KW   faecal streptococci; soil; sputum; biopsy; urine; food; pharmaceutical;
KW   cosmetic; fluorescent in situ hybridisation; FISH; ss.
XX
OS   Streptococcus sp.
XX
PN   WO2002102824-A2.
XX
PD   27-DEC-2002.
XX
PF   19-JUN-2002; 2002WO-EP06809.
XX
PR   19-JUN-2001; 2001DE-1029411.
PR   11-DEC-2001; 2001DE-1060666.
XX
PA   (VERM-) VERMICON AG.
XX
PI   Beimfohr C,  Snaidr J;
XX
DR   WPI; 2003-167479/16.
XX
PT   New oligonucleotides, useful for detecting bacteria that may
PT   contaminate drinking water, provide quick results for many species in
PT   parallel -
XX
PS   Claim 8; Page 12; 53pp; German.
XX
CC   This invention describes novel oligonucleotide probes used to detect
CC   contaminant bacteria that may be present in drinking water. The probes
CC   can detect bacteria (especially Legionella, faecal streptococci and
CC   coliforms) that may contaminate drinking water in environmental samples
CC   (water or soil), clinical samples (sputum, biopsies, urine etc.), in
CC   bathing and drinking water and in foods, pharmaceuticals and cosmetics,
CC   by in situ hybridisation. The probes combine the advantages of
CC   fluorescent in situ hybridisation with those of culture methods. Only a
CC   relatively short culture step is required; analysis takes 24-48 hours
CC   (contrast many days for conventional methods) and all relevant bacteria
CC   can be tested simultaneously. The oligonucleotides can differentiate
CC   between species of the same genus and are easy to use, allowing simple
CC   analysis of a large number of samples. ABX94532-ABX94578 represent the
CC   oligonucleotide probes described in the invention.
XX
SQ   Sequence 19 BP; 1 A; 7 C; 2 G; 9 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 25;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          4 CTTCTCTTTT 13


RESULT 33
AAT76779
ID   AAT76779 standard; DNA; 20 BP.
XX
AC   AAT76779;
XX
DT   15-SEP-1997  (first entry)
XX
DE   Staphylococcus aureus exfoliative toxin A gene PCR primer ETA-B.
XX
KW   Asymmetric polymerase chain reaction; nucleic acid amplification;
KW   PCR; detection; assay; exfoliative toxin A; ETA; skin lesion;
KW   competitive primer; capture probe; ss.
XX
OS   Synthetic.
XX
PN   US5627054-A.
XX
PD   06-MAY-1997.
XX
PF   05-APR-1996;   96US-0628417.
XX
PR   05-APR-1996;   96US-0628417.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Gillespie D;
XX
DR   WPI; 1997-271311/24.
XX
PT   Quantitative nucleic acid amplification - by competitor primer
PT   asymmetric polymerase chain reaction
XX
PS   Example 1; Column 5; 9pp; English.
XX
CC   In a specific example of a novel process for amplifying an amount
CC   (known or unknown) of a double-stranded nucleic acid segment to produce
CC   single-stranded nucleic acid in an amount that is proportional to the
CC   starting amount of the nucleic acid, the Staphylococcus aureus
CC   exfoliative toxin A (ETA) gene was used as the DNA template. The
CC   region comprising nucleotides 165-436 was amplified by symmetric,
CC   asymmetric or competitor primer asymmetric PCR using the primers
CC   ETA-A2 and ETA-B (see AAT76778 and AAT76779). For asymmetric PCR, the
CC   amount of primer ETA-B was reduced and for competitor primer
CC   asymmetric PCR a competitor primer ETA-B2 (see AAT76780) was added
CC   with upstream primer ETA-A2 after the initial cycling reaction. PCR
CC   products containing ETA-specific sequences were detected
CC   radioactively by a capture system which employed a bifunctional
CC   capture probe ETA-CP (see AAT76781 and AAT76782). ETA-CP was designed
CC   to capture the amplified sense strand onto capture membranes
CC   through hybridisation between the first 40 nucleotides of ETA-CP
CC   and nucleotides 321-360 of the ETA gene and through hybridisation
CC   of the poly(dA) tail on ETA-CP with poly(dT) tails on the capture
CC   membranes. A radioactively labelled "label probe" (see AAT76783),
CC   complementary to nucleotides 389-410 of the ETA gene was used to
CC   detect the amplicons. Results showed that hybridisation of the
CC   capture probe and label probe to the denatured symmetric PCR
CC   product was much less efficient than hybridisation to the
CC   single-stranded PCR products of the asymmetric and competitor
CC   primer asymmetric reactions.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17
```

RESULT 34
AAZ04007
ID AAZ04007 standard; DNA; 20 BP.
XX
AC AAZ04007;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB01939.
XX
PR 04-NOV-1998; 98US-0107077.
PR 28-NOV-1997; 97FR-0015041.
PR 17-DEC-1997; 97FR-0016034.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis
XX
PS Disclosure; Page 1653; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal uretritis, epidymitis, cervicitis, salpingitis,
CC perihepatitis, bartholinitis; pneumopathy in breast feeding infants;
CC and venereal lymphogranulomatosis. The polypeptides of the
CC invention may be of use in treating these diseases.
XX
SQ Sequence 20 BP; 0 A; 7 C; 3 G; 10 T; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 3 CTTCTCTTTT 12

RESULT 35
AAX97056/c
ID AAX97056 standard; DNA; 20 BP.
XX
AC AAX97056;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 1874; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotides sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 20 BP; 8 A; 4 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 17 CTTCTCTTTT 8

RESULT 36
AAL51617/c
ID AAL51617 standard; DNA; 20 BP.
XX
AC AAL51617;
XX
DT 17-APR-2003 (first entry)
XX
DE Human interferon alpha 2 sequencing primer #5.
XX
KW Human; ss; cellular proliferation inhibitor; interferon alpha 2;
KW single nucleotide polymorphism; SNP; cancer; tumour; metabolic disease;
KW cardiovascular disease; infectious disease; immunological disease; HIV;
KW central nervous system disease; wound healing; chemotherapy side effect;
KW anaemia; osteoporosis; gastrointestinal disease; venereal disease; AIDS;
KW obesity; hepatitis; infectious pneumonia; Alzheimer's disease; allergy;
KW Parkinson's disease; multiple sclerosis; schizophrenia; depression;
KW graft versus host disease; asthma; psoriasis; rheumatoid arthritis;
KW Crohn's disease; ulcerative colitis; genital wart; sequencing; primer.
XX
OS Homo sapiens.
XX
PN EP1236800-A2.

XX
PD 04-SEP-2002.
XX
PF 01-MAR-2002; 2002EP-0290515.
XX
PR 01-MAR-2001; 2001FR-0002843.
XX
PA (GENO-) GENODYSSEE.
XX
PI Escary J;
XX
DR WPI; 2003-185789/19.
XX
PT An isolated polynucleotide encoding interferon alpha 2 containing
PT single nucleotide polymorphisms is useful in treating disease -
XX
PS Example 4; Page 21; 42pp; English.
XX
CC The invention comprises the amino acid and coding sequence of the human
CC interferon alpha 2 protein. The invention further relates to the
CC identification of single nucleotide polymorphisms (SNPs) within the human
CC interferon alpha 2 gene. The DNA and protein sequences of the invention
CC are useful for the treatment of: cancer; tumours; cardiovascular
CC diseases; metabolic diseases; infectious diseases; central nervous system
CC diseases; immunological diseases; wound healing; chemotherapy side
CC effects; anaemia; osteoporosis; gastrointestinal diseases; venereal
CC diseases; obesity; hepatitis; HIV/AIDS; infectious pneumonias;
CC Alzheimer's disease; Parkinson's disease; multiple sclerosis;
CC schizophrenia; depression; graft versus host disease; allergies; asthma;
CC psoriasis; rheumatoid arthritis; Crohn's disease; ulcerative colitis; and
CC genital warts. The present DNA sequence represents a primer that was used
CC to sequence the human interferon alpha 2 gene.
XX
SQ Sequence 20 BP; 14 A; 1 C; 5 G; 0 U; 0 other;

Query Match 100.0%; Score 10; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 20 CTTCTCTTTT 11

RESULT 37
AAX60140/c
ID AAX60140 standard; DNA; 21 BP.
XX
AC AAX60140;
XX
DT 05-AUG-1999 (first entry)
XX
DE PCR primer used to amplify Mycoplasma hyopneumoniae P102 protein DNA.
XX
KW P102 protein; vaccine; antigen; diagnosis; swine; immunisation;
KW enzootic pneumonia; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9926664-A1.
XX
PD 03-JUN-1999.
XX
PF 24-NOV-1998; 98WO-US25044.
XX
PR 26-NOV-1997; 97US-0066565.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Hsu T, Minion FC;
XX
DR WPI; 1999-357741/30.
XX
PT Recombinant antigenic Mycoplasma hyponeumoniae protein
XX
PS Example 2; Page 23; 45pp; English.
XX
CC PCR primers AAX60140-41 were used to amplify DNA encoding a Mycoplasma
CC hyopneumoniae P102 protein clone. The P102 protein and its fragments
CC are used in vaccines to protect against enzootic pneumonia,
CC particularly in swine. Recombinant P102 polypeptides may be used as
CC antigens for diagnostic purposes to determine whether or not a
CC biological test sample contains M. hyponeumoniae antigens or
CC antibodies. The P102 polypeptides or DNA sequences may also be used
CC for immunising or protecting non-human animals, preferably swine,
CC against M. hyponeumoniae infections, particularly enzootic pneumonia.
XX
SQ Sequence 21 BP; 12 A; 0 C; 7 G; 2 T; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 15 CTTCTCTTTT 6

RESULT 38
AAV08126/c
ID AAV08126 standard; DNA; 21 BP.
XX
AC AAV08126;
XX
DT 22-JAN-1999 (first entry)
XX
DE Primer Vbeta14 for T cell receptor V region.
XX
KW PCR primer; T-cell receptor; TCR; V region; immune response; arthritis;
KW somatic homologous recombination; hypervariable region;
KW spectratype determination; autoimmune response; multiple sclerosis;
KW myasthenia gravis; muscular dystrophy; graft-infiltrating lymphocyte;
KW tumour-infiltrating lymphocyte; ss.
XX
OS Synthetic.
OS Mammalia.
XX
PN US5837447-A.
XX
PD 17-NOV-1998.
XX
PF 19-APR-1994; 94US-0229528.
XX
PR 19-APR-1994; 94US-0229528.
PR 15-APR-1992; 92US-0868569.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI Gorski J;
XX
DR WPI; 1999-023435/02.
XX
PT Monitoring immune responses by analysing amplified B or T-cell
PT nucleic acid - using primers specific for variable and constant or
PT junction region gene segments, with separation of products by
PT length, especially to monitor auto:immunity
XX
PS Claim 22; Column 38; 26pp; English.
XX
CC This sequence represents a primer for the T cell receptor (TCR) variable
CC region and is used in the method of the invention. The method is for
CC monitoring an immune response that involves somatic homologous
CC recombination between elements of at least two segments associated with a
CC hypervariable region, and comprises: (a) providing a polynucleotide
CC sample from B- or T-cells, and amplifying it with: (i) a primer specific
CC for a variable gene segment; and (ii) a primer specific for a constant or

```
CC   joining gene segment to produce amplification products (AP) that can be
CC   resolved at a difference in size of 2 or 3 bp; (c) separating the AP
CC   according to length; (d) detecting the range of lengths in the separated
CC   products to produce a 'spectratype' of the subject's immune response; and
CC   (e) comparing the spectratype with a predetermined standard to determine
CC   immune status or to monitor immune response. The method is specifically
CC   used to monitor autoimmune responses (including relapses), i.e. to
CC   identify the predominant TCR in sites of autoimmune activity (e.g. in
CC   arthritis, multiple sclerosis, myasthenia gravis and muscular dystrophy)
CC   or present in graft-infiltrating (in cases of organ rejection) or
CC   tumour-infiltrating lymphocytes. As each gene rearrangement is unique,
CC   each complementarity determining region 3 is a specific molecular
CC   fingerprint of the lymphocyte that generates it, and immune responses can
CC   be correlated with an increase in a particular TCR or immunoglobulin.
CC   Specific determination of two V beta families may be done simultaneously.
XX
SQ   Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 20;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 39
AAA95613/c
ID   AAA95613 standard; DNA; 21 BP.
XX
AC   AAA95613;
XX
DT   31-JAN-2001  (first entry)
XX
DE   TCR Vbeta 14 subfamily probe VB14-1.
XX
KW   Detection; diagnostic; Kawasaki disease; T-cell; PCR primer; probe;
KW   gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000157297-A.
XX
PD   13-JUN-2000.
XX
PF   01-DEC-1998;   98JP-0341661.
XX
PR   01-DEC-1998;   98JP-0341661.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
DR   WPI; 2000-477722/42.
XX
PT   Detection of Kawasaki disease factor, useful for the diagnosis of
PT   Kawasaki disease, comprises detecting an increase in Vbeta6.5 positive
PT   T-cells -
XX
PS   Example 1; Page 9; 36pp; Japanese.
XX
CC   The invention relates to a method of detecting Kawasaki disease by
CC   detecting an increase in Vbeta6.5 or Vbeta6.5/Vbeta2.1 positive T-cells.
CC   The sequences AAA95531-A95626 represent primers and probes used to PCR
CC   amplify and detect the level of expression of Valpha and Vbeta genes
CC   in T-cells in Kawasaki disease.
XX
SQ   Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 21;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 40
AAH27157/c
ID   AAH27157 standard; DNA; 21 BP.
XX
AC   AAH27157;
XX
DT   08-AUG-2001  (first entry)
XX
DE   Downstream PCR primer for amplification of PDAT gene.
XX
KW   Yeast; ARE 1; YCR048w; transgenic plant; oil production; acyl-CoA;
KW   fatty acid production; triacylglycerol; oil crop; rape; sunflower; PDAT;
KW   oil palm; soy; maize; oat; potato; sugar beet; turnip; PCR primer; ss.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200134814-A1.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-SE02216.
XX
PR   12-NOV-1999;   99EP-0850169.
PR   12-NOV-1999;   99US-0164859.
XX
PA   (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI   Banas A,  Sandager L,  Stahl U,  Dahlqvist A,  Lenman M,  Ronne H;
PI   Stymne S;
XX
DR   WPI; 2001-329086/34.
XX
PT   Transforming oil-producing organisms with a gene encoding an
PT   acyl-CoA:diacylglycerol acyltransferase, useful to generate
PT   agricultural crops with higher triacylglycerol content -
XX
PS   Example 1; Page 6; 30pp; English.
XX
CC   This invention relates to the use of a novel enzyme in the production of
CC   an oil-producing organism. The enzyme catalyses the transfer of a fatty
CC   acid from acyl-CoA to diacylglycerol to produce triacylglycerol,
CC   resulting in an increased oil content. Sequences AAH27155 and AAB97263
CC   represent the Saccharomyces cerevisiae ARE1 coding and protein sequence
CC   respectively. ARE1 is used in the transformation or the organism of the
CC   invention. The invention is used to increase the oil content of oil crops
CC   such as rape, sunflower and oil palm, and other crops such as soy, maize,
CC   oat, potato, sugar beet and turnips. The invention could also be used to
CC   produce triacylglycerols in microorganisms. The present sequence
CC   represents a PCR primer used to amplify the Saccharomyces cerevisiae PDAT
CC   gene. The primer and PCR product are used in an example illustrating that
CC   triacylglycerol accumulation is reduced in yeast cells that lack the ARE1
CC   gene. The primer is specifically used in the production of mutant yeast
CC   strains.
XX
SQ   Sequence 21 BP; 13 A; 3 C; 5 G; 0 U; 0 other;

  Query Match             100.0%;  Score 10;  DB 22;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 41
AAS95067/c
ID   AAS95067 standard; DNA; 21 BP.
XX
```

AC AAS95067;
XX
DT 13-FEB-2002 (first entry)
XX
DE Human otoferlin exon PCR primer #32.
XX
KW Human; mouse; otoferlin; OTOF; brain; auditory function; PCR primer;
KW autosomal nonsyndromic prelingual deafness; DFNB9; ss.
XX
OS Homo sapiens.
XX
PN WO200170972-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-IB00578.
XX
PR 24-MAR-2000; 2000US-191738P.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Yasunaga S, Grati M, Cohen-Salmon M, El Amraoui A, Petit C;
PI Weil D;
XX
DR WPI; 2001-611499/70.
XX
PT Novel human gene Otoferlin, underlying an autosomal recessive
PT nonsyndromic prelingual deafness, DFNB9, and proteins encoded by the
PT gene, implicated in deafness -
XX
PS Claim 25; Page 17; 99pp; English.
XX
CC The invention relates to a purified polynucleotide (I) encoding a protein
CC sequence (II) encoded by a novel human gene, otoferlin (OTOF) or
CC the long human otoferlin isoform in brain. (I) was identified as
CC underlying an autosomal nonsyndromic prelingual deafness DFNB9, and is
CC thus useful for detecting deafness disease in humans and for
CC characterising the functions of proteins and genes encoding them in
CC auditory function. AAS95022-AAS95248 represent human and mouse
CC otoferlin coding sequences, PCR primers and related sequences of the
CC invention.
XX
SQ Sequence 21 BP; 10 A; 1 C; 8 G; 2 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 10 CTTCTCTTTT 1

RESULT 42
AAX14678
ID AAX14678 standard; DNA; 22 BP.
XX
AC AAX14678;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 9-30 of gamma-crystallin gene.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Homo sapiens.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-0173489.
XX
PR 22-DEC-1993; 93US-0173489.
PR 29-OCT-1992; 92US-0968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria
XX
PS Disclosure; Columns 15-16; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX
SQ Sequence 22 BP; 1 A; 5 C; 0 G; 16 T; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 6 CTTCTCTTTT 15

RESULT 43
AAC66394/c
ID AAC66394 standard; DNA; 22 BP.
XX
AC AAC66394;
XX
DT 26-FEB-2001 (first entry)
XX
DE Human 3-hydroxyacyl-CoA-dehydratase cDNA specific PCR primer.
XX
KW Human; 3-hydroxyacyl-CoA-dehydratase; HCDase; hypothalamus;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1263157-A.
XX
PD 16-AUG-2000.
XX
PF 17-FEB-2000; 2000CN-0111690.
XX
PR 17-FEB-2000; 2000CN-0111690.
XX
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI Li N, Qian B, Peng Y;
XX
DR WPI; 2000-639262/62.
XX
PT New human hydroxybutyryl coenzyme A dehydratase protein and its coding
PT sequence -

```
XX
PS   Example 1; Page 11; 21pp; Chinese.
XX
CC   This invention relates to a new human 3-hydroxyacyl-CoA-dehydratase
CC   (HCDase). The protein is expressed in normal hypothalamic tissue in
CC   humans. The invention includes human HCDase nucleotide and amino acid
CC   sequences, a method for the preparation of the protein and a method for
CC   detecting human HCDase nucleic acid and protein sequences in a sample.
CC   The present sequence represents a PCR primer specific for human HCDase
CC   cDNA.
XX
SQ   Sequence 22 BP; 10 A; 2 C; 8 G; 2 T; 0 other;

  Query Match            100.0%;  Score 10;  DB 21;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 44
ABL35686
ID   ABL35686 standard; DNA; 22 BP.
XX
AC   ABL35686;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 612.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory;
KW   vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1..22
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18276.
XX
PR   07-JUN-2000; 2000US-209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection  -
XX
PS   Example 11; Page 63; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a
CC   bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence
CC   is an immunostimulatory oligonucleotide described in the exemplification
CC   of the invention.
XX
SQ   Sequence 22 BP; 1 A; 4 C; 3 G; 14 T; 0 other;

  Query Match            100.0%;  Score 10;  DB 24;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 45
ABL35687
ID   ABL35687 standard; DNA; 22 BP.
XX
AC   ABL35687;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 613.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory;
KW   vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1..22
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18276.
XX
PR   07-JUN-2000; 2000US-209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection  -
XX
PS   Example 11; Page 63; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
```

```
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a
CC   bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence
CC   is an immunostimulatory oligonucleotide described in the exemplification
CC   of the invention.
XX
SQ   Sequence 22 BP; 1 A; 4 C; 4 G; 13 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 46
ABL35688
ID   ABL35688 standard; DNA; 22 BP.
XX
AC   ABL35688;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 614.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory;
KW   vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1..22
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US18276.
XX
PR   07-JUN-2000; 2000US-209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection  -
XX
PS   Example 11; Page 63; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a
CC   bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence
CC   is an immunostimulatory oligonucleotide described in the exemplification
CC   of the invention.
XX
SQ   Sequence 22 BP; 1 A; 4 C; 2 G; 15 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 47
AAX10022/c
ID   AAX10022 standard; DNA; 23 BP.
XX
AC   AAX10022;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic marker downstream primer #328.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US20313.
XX
PR   06-NOV-1996;   96US-0030455.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Hudson T,  Lander ES,  Wang D;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease
XX
PS   Claim 16; Page 92; 310pp; English.
XX
CC   AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC   isolation of various biallelic polymorphic markers found in the human
CC   genome (represented in AAX10269-X12937). These primers can be used in a
CC   method for determining polymorphic forms in an individual for use in
CC   e.g. forensics, paternity testing or for phenotypic typing for diseases
CC   such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome,
CC   muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC   hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases.
XX
```

```
SQ   Sequence 23 BP; 16 A; 0 C; 7 G; 0 U; 0 other;

  Query Match             100.0%;  Score 10;  DB 19;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 48
AAQ50920/c
ID   AAQ50920 standard; DNA; 24 BP.
XX
AC   AAQ50920;
XX
DT   25-MAR-2003  (updated)
DT   19-MAY-1994  (first entry)
XX
DE   T-cell antigen receptor V-beta14 PCR primer.
XX
KW   RT-PCR; polymerase chain reaction; amplification; SSCP;
KW   single-strand conformation polymorphism; variable domain;
KW   subtype beta 14; ss.
XX
OS   Synthetic.
XX
PN   WO9322455-A1.
XX
PD   11-NOV-1993.
XX
PF   30-APR-1993;   93WO-JP00577.
XX
PR   30-APR-1992;   92JP-0111467.
PR   31-JUL-1992;   92JP-0205054.
XX
PA   (LTTL-) LTT INST CO LTD.
PA   (TAIS ) TAISHO PHARM CO LTD.
XX
PI   Ikeda Y,  Mizushima Y,  Nishioka K,  Sakoda H,  Yamamoto K;
XX
DR   WPI; 1993-368813/46.
XX
PT   Detection of expression of T-cell antigen receptor gene - in
PT   cancer, viral or immune disease patients, by polymerase chain
PT   reaction amplification of the gene and SSCP analysis
XX
PS   Claim 4; Page 13; 47pp; Japanese.
XX
CC   Primers corresp. to DNA coding for part of the beta-chain of the T
CC   cell antigen receptor (pref. the Variable region primers AAQ50905-
CC   AAQ50926) are used in PCR to amplify the T cell antigen receptor gene.
CC   The amplified gene is detected by the single-strand conformation
CC   polymorphism method using hybridisation probes corresp. to the
CC   beta-chain J domain (see AAQ50928-Q50940).
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 14;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 49
AAT10390/c
ID   AAT10390 standard; cDNA; 24 BP.
XX
AC   AAT10390;
XX
DT   02-APR-1996  (first entry)
XX
DE   T-cell receptor primer Vbeta14.
XX
KW   T cell receptor; beta chain; variable region; rheumatoid arthritis;
KW   synovial joint fluid; PCR; amplification; primer; immunogen; vaccine;
KW   immune disease; ss.
XX
OS   Synthetic.
XX
PN   WO9523164-A1.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-EP00670.
XX
PR   23-FEB-1994;   94EP-0200454.
XX
PA   (ALKU ) AKZO NOBEL NV.
XX
PI   Graus JPM,  Rijnders AWM,  Van Der Maaden JM;
XX
DR   WPI; 1995-311502/40.
XX
PT   Peptide contained in the variable region of a T-cell receptor beta
PT   chain - specifically associated with immune disease, esp. rheumatoid
PT   arthritis
XX
PS   Example 2; Page 24; 55pp; English.
XX
CC   The primers AAT10352-97 were used to PCR amplify the T cell receptor
CC   beta chain variable regions from T cell culture clones, isolated from
CC   the synovial joint fluid of 11 patients suffering from rheumatoid
CC   arthritis. The coding sequences were shown to contain the nucleotide
CC   sequence AAT07409.  The encoded polypeptide can be used as an immunogenic
CC   cpd. for the detection of or predisposition to an immune disease, or for
CC   use as a vaccine for prevention or treatment of an immune disease. This
CC   primer amplifies the variable region from the 14.1 family of clones.
XX
SQ   Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 16;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 50
AAT98116/c
ID   AAT98116 standard; DNA; 24 BP.
XX
AC   AAT98116;
XX
DT   13-MAR-1998  (first entry)
XX
DE   Primer V-beta(14) for T-cell receptor beta chain variable region.
XX
KW   Antibody; T-cell receptor; beta chain; human immunodeficiency virus;
KW   HIV; blood; attenuation; primer; PCR; amplification; variable region;
KW   constant region; TCR; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5665355-A.
XX
PD   09-SEP-1997.
XX
```

PF 07-JUN-1995; 95US-0488212.
XX
PR 09-NOV-1992; 92US-0973485.
PR 18-OCT-1994; 94US-0408011.
PR 07-JUN-1995; 95US-0488212.
XX
PA (CONS-) CONSORZIO BIOTECNOLOGIE.
XX
PI Primi D;
XX
DR WPI; 1997-456759/42.
XX
PT Removal of T-cell receptor-specific antibody from blood of
PT HIV-infected person - by extracorporeal blood treatment, to
PT attenuate or avert development of AIDS from HIV infection
XX
PS Example 1; Column 11; 43pp; English.
XX
CC The invention relates to a method for removing an antibody specific for
CC TCR-V beta (T-cell receptor V beta protein) from an HIV-infected person
CC by removing blood from the person, removing the antibody from the blood,
CC and reintroducing the blood into the person, thus allowing attenuation
CC or aversion of immunodeficiency. The primers AAT98100-T98150 are used
CC to check the efficiency of removal by detecting expression of the
CC TCR-V-beta and V-alpha genes in a blood sample after treatment. This
CC primer is targetted to the variable region sequence and can be used in
CC the amplification with primer AAT98100.
XX
SQ Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 51
AAX85959/c
ID AAX85959 standard; DNA; 24 BP.
XX
AC AAX85959;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify T cell receptor beta-chain cDNA.
XX
KW Acquired immune deficiency syndrome; free antibody; paratope; epitope;
KW T cell receptor variable beta region; TCR-V beta region; binding agent;
KW CD4+ T cell; HIV; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5928642-A.
XX
PD 27-JUL-1999.
XX
PF 18-OCT-1994; 94US-0408011.
XX
PR 09-NOV-1992; 92US-0973485.
PR 18-OCT-1994; 94US-0408011.
XX
PA (CONS-) CONSORZIO BIOTECNOLOGIE.
XX
PI Primi D;
XX
DR WPI; 1999-429481/36.
XX
PT Diagnosis and treatment of acquired immune deficiency syndrome
XX
PS Example 1; Column 11; 42pp; English.
XX
CC The specification describes a method for the diagnosis and treatment of
CC acquired immune deficiency syndrome, in a person having free antibodies
CC which have a paratope capable of binding to an epitope of a T cell
CC receptor variable beta (TCR-V beta) region. The method comprises
CC administering a binding agent homologous with the TCR-V beta
CC epitope. The binding agent is useful in assays for detecting various
CC CD4+ T cell subpopulations which carry particular V beta components.
CC The binding agent is also useful in the treatment of people infected
CC with HIV where it is able to remove an antibody able to bind with an
CC epitope on a TCR-V beta cell in the blood of an infected person. PCR
CC primers AAX85943-71 represent T cell receptor beta-chain primers used
CC in the course of the invention.
XX
SQ Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 52
AAX88135/c
ID AAX88135 standard; DNA; 24 BP.
XX
AC AAX88135;
XX
DT 09-SEP-1999 (first entry)
XX
DE T cell receptor beta chain primer V-beta14.
XX
KW T cell receptor; beta chain; primer; antibody; paratope; AIDS; vaccine;
KW epitope; TCR-V beta; immunogenic; anti-idiotypic; antiviral; detection;
KW CD4+ cell subpopulation; acquired immune deficiency syndrome; ss.
XX
OS Synthetic.
XX
PN US5925513-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-0488209.
XX
PR 09-NOV-1992; 92US-0973485.
PR 18-OCT-1994; 94US-0408011.
PR 07-JUN-1995; 95US-0488209.
XX
PA (CONS-) CONSORZIO BIOTECNOLOGIE.
XX
PI Primi D;
XX
DR WPI; 1999-418267/35.
XX
PT Diagnosis and treatment of acquired immune deficiency syndrome onset
XX
PS Example 1; Column 11-12; 42pp; English.
XX
CC This invention describes novel method for binding free antibodies having
CC a paratope specific to an epitope on a T cell receptor (TCR-V beta)
CC while providing an immunogenic substance able to raise anti-idiotypic
CC antibodies which bind to free antibodies bound at the same paratope
CC specific to the epitope on the TCR-V beta and introducing this into a
CC person to raise anti-idiotypic antibodies. The products of the invention
CC have antiviral activity and can be used in vaccines. The specific
CC antibody binding affinities are useful in assays which detect the
CC presence of CD4+ cell subpopulations carrying particular V beta
CC components of the TCR-V beta in people infected with acquired immune
CC deficiency syndrome (AIDS). AAX88119-X88169 represents primers used in

```
CC   the method of the invention.
XX
SQ   Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 20;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 53
AAI99892/c
ID   AAI99892 standard; DNA; 24 BP.
XX
AC   AAI99892;
XX
DT   30-JAN-2002  (first entry)
XX
DE   Human dihydroorotase 11 PCR primer SEQ ID NO 4.
XX
KW   Human; dihydroorotase 11; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; malignant tumour; HIV; infection;
KW   human immunodeficiency virus; immunological disease; gene therapy;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200173054-A1.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-CN00421.
XX
PR   27-MAR-2000; 2000CN-0115157.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-602867/68.
XX
PT   New human dihydroorotase 11 for diagnosing and treating malignant
PT   tumour, haemopathy, human immunodeficiency virus infection, immunological
PT   diseases and various inflammations  -
XX
PS   Example 2; Page 17; 34pp; Chinese.
XX
CC   The invention relates to human dihydroorotase 11 with  cytostatic,
CC   virucidal, immunomodulatory, antiinflammatory and haemostatic
CC   activity. The protein and encoding polynucleotide are used in diagnosis
CC   and treatment of malignant tumour, haemopathy, human immunodeficiency
CC   virus (HIV) infection, immunological diseases and various
CC   inflammations. The polynucleotide is useful in gene therapy. The present
CC   sequence is that of a PCR primer, useful to the invention.
XX
SQ   Sequence 24 BP; 8 A; 3 C; 8 G; 5 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 22;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 54
AAH19640/c
ID   AAH19640 standard; DNA; 24 BP.
XX
AC   AAH19640;
XX
DT   01-AUG-2001  (first entry)
XX
DE   Melon fusarium wilt-resistance marker FM forward primer FM-1.
XX
KW   Melon; cucurbit; Fusarium wilt; infection; resistance; susceptibility;
KW   genotype identification; polymerase chain reaction; PCR;
KW   Fusarium oxysporum; marker; PCR primer; ss.
XX
OS   Cucumis melo.
XX
PN   WO200127332-A1.
XX
PD   19-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US28633.
XX
PR   13-OCT-1999;   99US-0417722.
XX
PA   (UYCL-) UNIV CLEMSON.
XX
PI   Dean RA,  Wang Y;
XX
DR   WPI; 2001-300220/31.
XX
PT   Identifying cucurbit genotypes to determine susceptibility or
PT   resistance to Fusarium wilt disease, comprises using the polymerase
PT   chain reaction (PCR) and comparing the PCR product with known
PT   resistant/susceptible genotypes -
XX
PS   Claim 10; Fig 2; 36pp; English.
XX
CC   The present sequence is a primer used in a method for identifying
CC   genotypes in cucurbit plants, particularly species of melon, that
CC   are resistant or susceptible to Fusarium wilt disease. The method
CC   comprises extracting genomic DNA from a plant sample and using
CC   polymerase chain reaction (PCR) to produce DNA products for
CC   comparison with known DNA sequences of Fusarium-resistant/susceptible
CC   genotypes. The method is especially useful for establishing whether
CC   cucurbit plants are resistant or susceptible to Fusarium wilt
CC   disease caused by Fusarium oxysporum infection. The method uses PCR
CC   to detect the genotypes. PCR is sensitive and accurate, and it is a
CC   much more rapid procedure than previous methods such as artificial
CC   inoculation (AI). The new method is also more cost effective and
CC   more suitable for high through-put analysis.
CC   Note: The present sequence is given as SEQ ID NO: 3 in Figure 2,
CC   but it is different to the sequence given as SEQ ID NO: 3 in the
CC   sequence listing.
XX
SQ   Sequence 24 BP; 14 A; 1 C; 8 G; 1 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 22;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 55
ABS71673/c
ID   ABS71673 standard; DNA; 24 BP.
XX
AC   ABS71673;
XX
DT   28-NOV-2002  (first entry)
XX
DE   T cell receptor (TCR) variable beta (BV) peptide RT-PCR primer #16.
XX
KW   T cell receptor; TCR; receptor; variable beta peptide; BV peptide; TCRV;
KW   T cell variable gene; T cell regulatory activity; autoimmune disease;
```

KW multiple sclerosis; human; reverse transcriptase; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002107388-A1.
XX
PD 08-AUG-2002.
XX
PF 10-MAY-2001; 2001US-0853830.
XX
PR 12-MAY-2000; 2000US-203984P.
XX
PA (VAND/) VANDENBARK A A.
XX
PI Vandenbark AA;
XX
DR WPI; 2002-697882/75.
XX
PT Identifying a T cell receptor variable gene expressed by target T cells
PT in an individual is useful to identify disease-associated T cells for
PT design of individualised therapies, particularly for autoimmune disease
PT -
XX
PS Example 2; Page 11; 20pp; English.
XX
CC The invention relates to a method for identifying a T cell receptor
CC variable (TCRV) gene expressed by target T cells in an individual,
CC comprising determining expression of TCRV genes by activated T cells from
CC the individual and determining regulatory activity elicited in response
CC to TCRV peptides from the individual. A preferentially expressed TCRV
CC gene whose TCRV peptide elicits low T cell regulatory activity is
CC identified as a variable gene expressed by target T cells. The method is
CC used to identify disease-associated T cells in an individual so that
CC individualised therapies can be designed to prevent or treat the disease,
CC particularly an autoimmune disease, especially multiple sclerosis. This
CC sequence represents a reverse transcriptase PCR (RT-PCR) primer used in
CC analysis of expression of DNA encoding TCR variable beta (BV) peptides.
XX
SQ Sequence 24 BP; 10 A; 3 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 56
ABK67667/c
ID ABK67667 standard; DNA; 24 BP.
XX
AC ABK67667;
XX
DT 02-JUL-2002 (first entry)
XX
DE B. subtilis knock-out PCR primer KO murA R1.
XX
KW Antibacterial; antiprotozoal; antifungal; cell growth inhibitor;
KW protozoa; bacterium; fungus; amoeba; mycoplasma; murA;
KW folA; yibD; primer; ss.
XX
OS Bacillus subtilis.
XX
PN WO200216940-A2.
XX
PD 28-FEB-2002.
XX
PF 23-AUG-2001; 2001WO-US26322.
XX
PR 23-AUG-2000; 2000US-226896P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Sulavik M, Ling LL, Opperman T, Moir DT, Bunker C;
XX
DR WPI; 2002-329705/36.
XX
PT Identification of a molecular target of a cell growth inhibitor,
PT comprises target prediction processes to identify at least one
PT modulated gene or gene product -
XX
PS Example 2; Page 97; 157pp; English.
XX
CC The invention relates to a method of identifying a molecular target of a
CC cell growth inhibiting compound by: (a) identifying a compound or
CC composition inhibiting growth in a population of cells; (b) performing
CC target prediction processes to identify a modulated gene or gene product;
CC and (c) comparing by target prediction process with the gene or gene
CC product identified by other prediction processes. The method is used for
CC identifying the molecular target of a cell growth inhibitor. The cells
CC are selected from organisms such as protozoa, bacterium, fungus, amoeba
CC and mycoplasma. The method reaps the benefits of both cell-based and
CC target-based screening. The method relies first on identification of
CC compounds with good whole cell activity and then provides methods to
CC identify the target of the compounds. Each of the methods is successful
CC in isolation, but in combination of at least two (preferably at least
CC three) provides a higher success in identifying the molecular target.
CC ABK67622-ABK67679 represent PCR primers used in examples which
CC demonstrate the method of the invention.
XX
SQ Sequence 24 BP; 9 A; 4 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 16 CTTCTCTTTT 7

RESULT 57
ABA04339/c
ID ABA04339 standard; DNA; 24 BP.
XX
AC ABA04339;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human BolA structural domain zinc finger protein 37 PCR primer 1.
XX
KW Human; BolA structural domain zinc finger protein 37; malignant tumour;
KW nosohaemia; HIV infection; immunological disease; inflammation;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1307053-A.
XX
PD 08-AUG-2001.
XX
PF 28-JAN-2000; 2000CN-0111611.
XX
PR 28-JAN-2000; 2000CN-0111611.
XX
PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-062745/09.
XX
PT Polypeptide-human Bola structural domain zinc finger protein 37 and
PT polynucleotide for said polypeptide -
XX

PS Example 3; Page 17 (Disclosure); 35pp; Chinese.
XX
CC The present invention describes human BolA structural domain zinc finger
CC protein 37 (I). (I) can be used in the treatment of various diseases,
CC such as malignant tumour, nosohaemia, HIV infection, immunological
CC diseases and inflammations. The present sequence represents a PCR primer
CC for human BolA structural domain zinc finger protein 37, which is used
CC in an example from the present invention.
XX
SQ Sequence 24 BP; 12 A; 4 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 58
ABL45589/c
ID ABL45589 standard; DNA; 24 BP.
XX
AC ABL45589;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 21q22.1 PCR primer SEQ ID NO:2633.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
KW genome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-0068285.
XX
PR 10-MAR-2000; 2000JP-0066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones -
XX
PS Claim 6; Page 57; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention.
XX
SQ Sequence 24 BP; 12 A; 2 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 19 CTTCTCTTTT 10

RESULT 59
AAT76780
ID AAT76780 standard; DNA; 25 BP.
XX
AC AAT76780;
XX
DT 15-SEP-1997 (first entry)
XX
DE Staphylococcus aureus exfoliative toxin A competitor primer ETA-B2.
XX
KW Asymmetric polymerase chain reaction; nucleic acid amplification;
KW PCR; detection; assay; exfoliative toxin A; ETA; skin lesion;
KW competitive primer; capture probe; ss.
XX
OS Synthetic.
XX
PN US5627054-A.
XX
PD 06-MAY-1997.
XX
PF 05-APR-1996; 96US-0628417.
XX
PR 05-APR-1996; 96US-0628417.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Gillespie D;
XX
DR WPI; 1997-271311/24.
XX
PT Quantitative nucleic acid amplification - by competitor primer
PT asymmetric polymerase chain reaction
XX
PS Example 1; Column 5; 9pp; English.
XX
CC In a specific example of a novel process for amplifying an amount
CC (known or unknown) of a double-stranded nucleic acid segment to produce
CC single-stranded nucleic acid in an amount that is proportional to the
CC starting amount of the nucleic acid, the Staphylococcus aureus
CC exfoliative toxin A (ETA) gene was used as the DNA template. The
CC region comprising nucleotides 165-436 was amplified by symmetric,
CC asymmetric or competitor primer asymmetric PCR using the primers
CC ETA-A2 and ETA-B (see AAT76778 and AAT76779). For asymmetric PCR, the
CC amount of primer ETA-B was reduced and for competitor primer
CC asymmetric PCR a competitor primer ETA-B2 (see AAT76780) was added
CC with upstream primer ETA-A2 after the initial cycling reaction. PCR
CC products containing ETA-specific sequences were detected
CC radioactively by a capture system which employed a bifunctional
CC capture probe ETA-CP (see AAT76781 and AAT76782). ETA-CP was designed
CC to capture the amplified sense strand onto capture membranes
CC through hybridisation between the first 40 nucleotides of ETA-CP
CC and nucleotides 321-360 of the ETA gene and through hybridisation
CC of the poly(dA) tail on ETA-CP with poly(dT) tails on the capture
CC membranes. A radioactively labelled "label probe" (see AAT76783),
CC complementary to nucleotides 389-410 of the ETA gene was used to
CC detect the amplicons. Results showed that hybridisation of the
CC capture probe and label probe to the denatured symmetric PCR
CC product was much less efficient than hybridisation to the
CC single-stranded PCR products of the asymmetric and competitor
CC primer asymmetric reactions.
XX

SQ Sequence 25 BP; 4 A; 5 C; 3 G; 8 T; 5 other;

Query Match 100.0%; Score 10; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 8 CTTCTCTTTT 17

RESULT 60
ABV82471/c
ID ABV82471 standard; DNA; 25 BP.
XX
AC ABV82471;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3717.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 551; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 2 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 25 CTTCTCTTTT 16

RESULT 61
ABV82472/c
ID ABV82472 standard; DNA; 25 BP.
XX
AC ABV82472;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3718.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 551; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are

CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 8 A; 2 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 24 CTTCTCTTTT 15

RESULT 62
ABV82473/c
ID ABV82473 standard; DNA; 25 BP.
XX
AC ABV82473;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3719.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 551; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 2 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 23 CTTCTCTTTT 14

RESULT 63
ABV82474/c
ID ABV82474 standard; DNA; 25 BP.
XX
AC ABV82474;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3720.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 551; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 2 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 22 CTTCTCTTTT 13

RESULT 64
ABV82475/c
ID ABV82475 standard; DNA; 25 BP.
XX
AC ABV82475;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3721.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 551; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 2 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 21 CTTCTCTTTT 12

RESULT 65
ABV82476/c
ID ABV82476 standard; DNA; 25 BP.
XX
AC ABV82476;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3722.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 551; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is

CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 2 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 20 CTTCTCTTTT 11

RESULT 66
ABV82477/c
ID ABV82477 standard; DNA; 25 BP.
XX
AC ABV82477;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3723.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 1 C; 8 G; 7 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 19 CTTCTCTTTT 10

RESULT 67
ABV82478/c
ID ABV82478 standard; DNA; 25 BP.
XX
AC ABV82478;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3724.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 1 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 68
ABV82479/c
ID ABV82479 standard; DNA; 25 BP.
XX
AC ABV82479;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3725.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 2 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 17 CTTCTCTTTT 8

RESULT 69
ABV82480/c
ID ABV82480 standard; DNA; 25 BP.
XX
AC ABV82480;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3726.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX

CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 3 C; 8 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 16 CTTCTCTTTT 7

RESULT 70
ABV82481/c
ID ABV82481 standard; DNA; 25 BP.
XX
AC ABV82481;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3727.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 15 CTTCTCTTTT 6

RESULT 71
ABV82482/c
ID ABV82482 standard; DNA; 25 BP.
XX
AC ABV82482;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3728.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding

PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 14 CTTCTCTTTT 5

RESULT 72
ABV82483/c
ID ABV82483 standard; DNA; 25 BP.
XX
AC ABV82483;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3729.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX

PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 13 CTTCTCTTTT 4

RESULT 73
ABV82484/c
ID ABV82484 standard; DNA; 25 BP.
XX
AC ABV82484;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3730.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX

DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 552; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 3 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 12 CTTCTCTTTT 3

RESULT 74
ABV82485/c
ID ABV82485 standard; DNA; 25 BP.
XX
AC ABV82485;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3731.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 553; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 11 CTTCTCTTTT 2

RESULT 75
ABV82486/c
ID ABV82486 standard; DNA; 25 BP.
XX
AC ABV82486;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 3732.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-0001167.
XX
PR 30-JAN-2001; 2001WO-US00663.
PR 30-JAN-2001; 2001WO-US00664.
PR 30-JAN-2001; 2001WO-US00665.
PR 30-JAN-2001; 2001WO-US00667.
PR 30-JAN-2001; 2001WO-US00668.
PR 30-JAN-2001; 2001WO-US00669.
PR 23-MAY-2001; 2001US-0864761.
PR 09-OCT-2001; 2001US-0327898.
XX

PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL),
PT useful for identifying agonist and antagonist and specific binding
PT partners, and for treating subjects having defects in HTPL -
XX
PS Example 2; Page 553; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention.
XX
SQ Sequence 25 BP; 9 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 10 CTTCTCTTTT 1

RESULT 76
ABS75576/c
ID ABS75576 standard; DNA; 25 BP.
XX
AC ABS75576;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1102.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 220; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 11 A; 3 C; 8 G; 3 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 25 CTTCTCTTTT 16

RESULT 77
ABS75577/c
ID ABS75577 standard; DNA; 25 BP.
XX
AC ABS75577;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1103.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 220; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or

```
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention.
XX
SQ   Sequence 25 BP; 11 A; 3 C; 8 G; 3 T; 0 other;

  Query Match            100.0%;  Score 10;  DB 24;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         24 CTTCTCTTTT 15


RESULT 78
ABS75578/c
ID   ABS75578 standard; DNA; 25 BP.
XX
AC   ABS75578;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1104.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-0827998.
XX
PR   26-MAY-2000; 2000US-207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy  -
XX
PS   Example 2; Page 220; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes
CC   one of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention.
XX
SQ   Sequence 25 BP; 11 A; 3 C; 7 G; 4 T; 0 other;

  Query Match            100.0%;  Score 10;  DB 24;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 79
ABS75579/c
ID   ABS75579 standard; DNA; 25 BP.
XX
AC   ABS75579;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1105.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-0827998.
XX
PR   26-MAY-2000; 2000US-207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy  -
XX
PS   Example 2; Page 220; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes
CC   one of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention.
XX
SQ   Sequence 25 BP; 12 A; 2 C; 7 G; 4 T; 0 other;

  Query Match            100.0%;  Score 10;  DB 24;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 80
ABS75580/c
ID   ABS75580 standard; DNA; 25 BP.
XX
AC   ABS75580;
```

XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1106.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 220; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 13 A; 2 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 21 CTTCTCTTTT 12

RESULT 81
ABS75581/c
ID ABS75581 standard; DNA; 25 BP.
XX
AC ABS75581;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1107.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 220; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 13 A; 2 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 20 CTTCTCTTTT 11

RESULT 82
ABS75582/c
ID ABS75582 standard; DNA; 25 BP.
XX
AC ABS75582;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1108.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX

DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 221; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 2 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 19 CTTCTCTTTT 10

RESULT 83
ABS75583/c
ID ABS75583 standard; DNA; 25 BP.
XX
AC ABS75583;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1109.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 221; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 3 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 84
ABS75584/c
ID ABS75584 standard; DNA; 25 BP.
XX
AC ABS75584;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1110.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 221; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 4 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;

```
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 85
ABS75585/c
ID   ABS75585 standard; DNA; 25 BP.
XX
AC   ABS75585;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1111.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-0827998.
XX
PR   26-MAY-2000; 2000US-207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy  -
XX
PS   Example 2; Page 221; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes
CC   one of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention.
XX
SQ   Sequence 25 BP; 12 A; 4 C; 4 G; 5 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 86
ABS75586/c
ID   ABS75586 standard; DNA; 25 BP.
XX
AC   ABS75586;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1112.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-0827998.
XX
PR   26-MAY-2000; 2000US-207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy  -
XX
PS   Example 2; Page 221; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes
CC   one of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention.
XX
SQ   Sequence 25 BP; 12 A; 4 C; 4 G; 5 T; 0 other;

  Query Match             100.0%;  Score 10;  DB 24;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 87
ABS75587/c
ID   ABS75587 standard; DNA; 25 BP.
XX
AC   ABS75587;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 25-mer SEQ ID 1113.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
```

PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 221; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 3 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 14 CTTCTCTTTT 5

RESULT 88
ABS75588/c
ID ABS75588 standard; DNA; 25 BP.
XX
AC ABS75588;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1114.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 221; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 3 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 13 CTTCTCTTTT 4

RESULT 89
ABS75589/c
ID ABS75589 standard; DNA; 25 BP.
XX
AC ABS75589;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1115.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 221; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic

CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 11 A; 3 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 12 CTTCTCTTTT 3

RESULT 90
ABS75590/c
ID ABS75590 standard; DNA; 25 BP.
XX
AC ABS75590;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1116.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 222; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 2 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 11 CTTCTCTTTT 2

RESULT 91
ABS75591/c
ID ABS75591 standard; DNA; 25 BP.
XX
AC ABS75591;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 25-mer SEQ ID 1117.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-0827998.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy -
XX
PS Example 2; Page 222; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes
CC one of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention.
XX
SQ Sequence 25 BP; 12 A; 2 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 10 CTTCTCTTTT 1

RESULT 92
AAQ45398/c
ID AAQ45398 standard; DNA; 27 BP.

XX
AC AAQ45398;
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1994 (first entry)
XX
DE Oligonucleotide forming triplex with viral polypurine tract.
XX
KW HIV; human immunodeficiency virus; retrovirus; hepadna virus;
KW reverse transcription; virus replication; inhibition; treatment;
KW therapy; polypurine; triplex; antisense; ss.
XX
OS Synthetic.
XX
PN WO9407367-A1.
XX
PD 14-APR-1994.
XX
PF 29-SEP-1993; 93WO-US09300.
XX
PR 29-SEP-1992; 92US-0954184.
XX
PA (APOL-) APOLLON INC.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Moelling K;
XX
DR WPI; 1994-135099/16.
XX
PT Antiviral oligomers that bind poly-purine tracts of
PT single-stranded RNA or RNA - DNA hybrids - used to target the
PT early stages of viral replication before double stranded DNA is
PT formed
XX
PS Example 4; Page 29; 54pp; English.
XX
CC Administration of antisense or triplex forming oligonucleotides
CC which bind polypurine tracts (PPT) may be used in the therapy or
CC treatment of individuals infected with retroviruses or hepadna
CC viruses since in these two families of viruses, two primers are
CC involved in the reverse transcription of viral RNA into double
CC stranded DNA, one of which is a PPT. The antisense or triplex
CC forming oligonucleotides can inhibit the early stages of viral
CC replication by binding to the PPT primer or by binding to PPT
CC tracts in the RNA-DNA hybrid molecule formed after reverse
CC transcription of the viral RNA. This oligonucleotide was incubated
CC with an in vitro transcribed 5' end labelled pKJ2 RNA of 134
CC nucleotides in length to which a 40-mer deoxyribonucleotide
CC complementary to the PPT had been hybridised. The presence of this
CC sequence led to protection of the pKJ2 RNA-DNA hybrid from RNase H
CC digestion which would suggest the formation of a triplex. Triplex
CC formation was confirmed using a primer extension technique. A
CC primer binding downstream of the PPT was synthesised and extended in
CC vitro by reverse transcriptase in the presence of
CC oligodeoxynucleotides including one which was radioactively labelled.
CC The newly synthesised DNA was terminated at the site of the PPT when
CC the triplex was formed and blocked extension. Triplex formation
CC would be expected to interfere with viral replication in vivo.
CC See AAQ45381-Q45417. This is a variant of the sequence described in
CC AAQ45387.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 27 BP; 7 A; 8 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 22 CTTCTCTTTT 13

RESULT 93
AAX74299/c
ID AAX74299 standard; RNA; 27 BP.
XX
AC AAX74299;
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flt-1 VEGF receptor hammerhead ribozyme #771.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US17480.
XX
PR 11-JAN-1996; 96US-0584040.
PR 26-OCT-1995; 95US-0005974.
XX
PA (CHIR) CHIRON CORP.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX
PS Claim 9; Page 178; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 27 BP; 12 A; 1 C; 9 G; 4 U; 1 other;

Query Match 100.0%; Score 10; DB 18; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 27 CTTCTCTTTT 18

RESULT 94
AAH62997
ID AAH62997 standard; DNA; 27 BP.
XX
AC AAH62997;
XX
DT 11-SEP-2001 (first entry)
XX
DE Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 158.
XX

KW Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW antiviral agent; gene expression; antisense construct; probe; primer;
KW transgenic viral resistant shrimp; ss.
XX
OS White spot syndrome virus.
XX
PN WO200138351-A2.
XX
PD 31-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US28888.
XX
PR 24-NOV-1999; 99CN-0124717.
XX
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
XX
PI Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
XX
DR WPI; 2001-355877/37.
XX
PT Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PT (WSBV), useful for producing viral polypeptides that can be used to
PT screen for agents that are useful for treating WSBV infection -
XX
PS Disclosure; Figure 3; 626pp; English.
XX
CC The invention provides the primary nucleotide sequence of the WSBV genome
CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
CC encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
CC molecules and proteins of the invention are useful for diagnosis and
CC monitoring viral infection, in screens for antiviral agents and for
CC monitoring viral gene expression or activity during a treatment regimen.
CC The nucleic acid molecules are also useful as antisense constructs to
CC control viral gene expression in infected cells and tissues and to create
CC transgenic viral resistant shrimp.
XX
SQ Sequence 27 BP; 5 A; 6 C; 2 G; 14 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 2 CTTCTCTTTT 11

RESULT 95
AAH38166/c
ID AAH38166 standard; DNA; 27 BP.
XX
AC AAH38166;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 962.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28436.
XX
PR 15-OCT-1999; 99US-0160096.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX
PS Claim 1; Page 54; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence.
XX
SQ Sequence 27 BP; 13 A; 5 C; 4 G; 5 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 21 CTTCTCTTTT 12

RESULT 96
AAC81508
ID AAC81508 standard; DNA; 28 BP.
XX
AC AAC81508;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human MSF exon 6 RT-PCR primer, SEQ ID NO:16.
XX
KW Human MSF; megakaryocyte stimulating factor; tribonectin;
KW alternative splicing; joint boundary lubricant; O-linked oligosaccharide;
KW osteoarthritis; tribosupplementation; tissue adhesion inhibition;
KW friction coefficient reduction; gene therapy; antiarthritic;
KW osteopathic; reverse transcription-PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200064930-A2.
XX
PD 02-NOV-2000.
XX

PF 24-APR-2000; 2000WO-US10953.
XX
PR 23-APR-1999; 99US-0298970.
XX
PA (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
XX
PI Jay GD;
XX
DR WPI; 2001-024673/03.
XX
PT Novel tribonectin polypeptide useful as lubricant for treating
PT osteoarthritis, comprises O-linked lubricating moiety -
XX
PS Example 1; Page 23; 47pp; English.
XX
CC The invention relates to a human tribonectin which is a product of
CC alternative splicing of the human MSF (megakaryocyte stimulating factor)
CC gene. The tribonectin has at least one O-linked oligosaccharide
CC lubricating moiety and has a polypeptide sequence comprising 1-76
CC repeats of a motif having at least 50% identity to the sequence KEPAPTT
CC (AAB29774). The invention also relates to a nucleic acid encoding a
CC human MSF-derived tribonectin; a biocompatible composition comprising a
CC human tribonectin for inhibiting tissue adhesion formation; and a method
CC of diagnosing osteoarthritis or a predisposition to osteoarthritis by
CC measuring the amount of MSF or its fragment in a biological sample of a
CC mammal, wherein an increased amount of MSF compared to a control
CC indicates the presence of or predisposition to developing
CC osteoarthritis. The tribonectin and DNA encoding it are useful in the
CC treatment of osteoarthritis, where they may be used for lubricating
CC mammalian joints, such as articulating joints of humans, dogs or horses.
CC The tribonectin, when formulated as a membrane, foam, gel or fibre, is
CC useful for inhibiting adhesion between two surfaces such as the injured
CC tissues of a mammal, where the injury is caused by a surgical insertion
CC or trauma, or an artificial device e.g., an orthopaedic implant. In
CC particular, one of the surfaces is pericardial tissue. DNA encoding a
CC tribonectin may be used in gene therapy. The present sequence represents
CC a human MSF gene reverse transcription-PCR (RT-PCR) primer used in an
CC exemplification of the invention.
XX
SQ Sequence 28 BP; 5 A; 7 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 12 CTTCTCTTTT 21

RESULT 97
AAF05757/c
ID AAF05757 standard; RNA; 29 BP.
XX
AC AAF05757;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme #2976.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US09721.
XX
PR 12-APR-1999; 99US-0129390.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, McSwiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor
PT protein, interferon alpha and erythropoietin -
XX
PS Claim 48; Page 124; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAATT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 29 BP; 10 A; 4 C; 9 G; 5 U; 1 other;

Query Match 100.0%; Score 10; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 29 CTTCTCTTTT 20

RESULT 98
AAA40663
ID AAA40663 standard; DNA; 29 BP.
XX
AC AAA40663;
XX
DT 15-AUG-2000 (first entry)
XX
DE Human CD36 polymorphism sequence variant oligonucleotide SEQ ID NO:133.
XX
KW Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis;
KW therapy; screening; polymorphism; variant; detection; mutant;
KW blood; mutation; insulin; glucose metabolism; fatty acid metabolism;
KW catecholamine; malaria; infection; parasite; antiparasitic;
KW antidiabetic; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200019883-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US23418.
XX
PR 07-OCT-1998; 98US-0167750.
PR 28-DEC-1998; 98US-0221222.
PR 17-MAR-1999; 99US-0270542.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (AITM/) AITMAN T J.
PA (SCOT/) SCOTT J.
PA (STAN/) STANTON L W.
XX
PI Aitman TJ, Scott J, Stanton LW;
XX
DR WPI; 2000-303596/26.
XX
PT Nucleic acids encoding mutant CD36 proteins useful for preventing,
PT diagnosing and treating parasitic infections, especially malaria -

XX
PS Claim 26; Page 90; 167pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (A)
CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium
CC falciparum (the major cause of malaria) are unable to utilise the
CC mutated proteins to gain entry to, and infect cells. The mutant CD36
CC proteins do not function correctly preventing parasites utilising them
CC to infect cells. The nucleic acids may be used for the recombinant
CC production of mutant CD36 proteins according to standard methodologies.
CC They may be used in this way to prevent and treat parasitic infections
CC that utilise the CD36 protein to infect cells, such as P. falciparum,
CC the major cause of malaria. For example, the protein may be used to
CC identify modulators of CD36 expression and activity or a patient's CD36
CC DNA may be screened to determine whether there are any mutations present
CC that may confer resistance to parasitic infections. The proteins and
CC nucleic acids may also be used to prevent, diagnose and treat diseases
CC associated with defects in insulin action and/or glucose metabolism
CC and/or fatty acid metabolism and/or catecholamine action in subjects
CC possessing mutations in the CD36 genes. AAA40606 to AAA40759, and
CC AAB02515 to AAB02564, represent nucleotide and amino acid sequences
CC respectively which are used in the exemplification of the present
CC invention.
XX
SQ Sequence 29 BP; 1 A; 5 C; 10 G; 13 T; 0 other;

Query Match 100.0%; Score 10; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 8 CTTCTCTTTT 17

RESULT 99
AAA40662
ID AAA40662 standard; DNA; 30 BP.
XX
AC AAA40662;
XX
DT 15-AUG-2000 (first entry)
XX
DE Human CD36 polymorphism sequence variant oligonucleotide SEQ ID NO:132.
XX
KW Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis;
KW therapy; screening; polymorphism; variant; detection; mutant;
KW blood; mutation; insulin; glucose metabolism; fatty acid metabolism;
KW catecholamine; malaria; infection; parasite; antiparasitic;
KW antidiabetic; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200019883-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US23418.
XX
PR 07-OCT-1998; 98US-0167750.
PR 28-DEC-1998; 98US-0221222.
PR 17-MAR-1999; 99US-0270542.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (AITM/) AITMAN T J.
PA (SCOT/) SCOTT J.
PA (STAN/) STANTON L W.
XX
PI Aitman TJ, Scott J, Stanton LW;
XX
DR WPI; 2000-303596/26.
XX
PT Nucleic acids encoding mutant CD36 proteins useful for preventing,
PT diagnosing and treating parasitic infections, especially malaria -
XX
PS Claim 26; Page 90; 167pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (A)
CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium
CC falciparum (the major cause of malaria) are unable to utilise the
CC mutated proteins to gain entry to, and infect cells. The mutant CD36
CC proteins do not function correctly preventing parasites utilising them
CC to infect cells. The nucleic acids may be used for the recombinant
CC production of mutant CD36 proteins according to standard methodologies.
CC They may be used in this way to prevent and treat parasitic infections
CC that utilise the CD36 protein to infect cells, such as P. falciparum,
CC the major cause of malaria. For example, the protein may be used to
CC identify modulators of CD36 expression and activity or a patient's CD36
CC DNA may be screened to determine whether there are any mutations present
CC that may confer resistance to parasitic infections. The proteins and
CC nucleic acids may also be used to prevent, diagnose and treat diseases
CC associated with defects in insulin action and/or glucose metabolism
CC and/or fatty acid metabolism and/or catecholamine action in subjects
CC possessing mutations in the CD36 genes. AAA40606 to AAA40759, and
CC AAB02515 to AAB02564, represent nucleotide and amino acid sequences
CC respectively which are used in the exemplification of the present
CC invention.
XX
SQ Sequence 30 BP; 1 A; 5 C; 10 G; 14 T; 0 other;

Query Match 100.0%; Score 10; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 8 CTTCTCTTTT 17

RESULT 100
AAA40664
ID AAA40664 standard; DNA; 30 BP.
XX
AC AAA40664;
XX
DT 15-AUG-2000 (first entry)
XX
DE Human CD36 polymorphism sequence variant oligonucleotide SEQ ID NO:134.
XX
KW Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis;
KW therapy; screening; polymorphism; variant; detection; mutant;
KW blood; mutation; insulin; glucose metabolism; fatty acid metabolism;
KW catecholamine; malaria; infection; parasite; antiparasitic;
KW antidiabetic; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200019883-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US23418.
XX
PR 07-OCT-1998; 98US-0167750.
PR 28-DEC-1998; 98US-0221222.
PR 17-MAR-1999; 99US-0270542.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
PA (SCIO-) SCIOS INC.
PA (AITM/) AITMAN T J.
PA (SCOT/) SCOTT J.
PA (STAN/) STANTON L W.
XX

PI Aitman TJ, Scott J, Stanton LW;
XX
DR WPI; 2000-303596/26.
XX
PT Nucleic acids encoding mutant CD36 proteins useful for preventing,
PT diagnosing and treating parasitic infections, especially malaria -
XX
PS Claim 26; Page 90; 167pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (A)
CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium
CC falciparum (the major cause of malaria) are unable to utilise the
CC mutated proteins to gain entry to, and infect cells. The mutant CD36
CC proteins do not function correctly preventing parasites utilising them
CC to infect cells. The nucleic acids may be used for the recombinant
CC production of mutant CD36 proteins according to standard methodologies.
CC They may be used in this way to prevent and treat parasitic infections
CC that utilise the CD36 protein to infect cells, such as P. falciparum,
CC the major cause of malaria. For example, the protein may be used to
CC identify modulators of CD36 expression and activity or a patient's CD36
CC DNA may be screened to determine whether there are any mutations present
CC that may confer resistance to parasitic infections. The proteins and
CC nucleic acids may also be used to prevent, diagnose and treat diseases
CC associated with defects in insulin action and/or glucose metabolism
CC and/or fatty acid metabolism and/or catecholamine action in subjects
CC possessing mutations in the CD36 genes. AAA40606 to AAA40759, and
CC AAB02515 to AAB02564, represent nucleotide and amino acid sequences
CC respectively which are used in the exemplification of the present
CC invention.
XX
SQ Sequence 30 BP; 1 A; 5 C; 10 G; 14 T; 0 other;

Query Match 100.0%; Score 10; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17
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Search completed: October 28, 2003, 17:17:58
Job time : 287 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 28, 2003, 15:14:10 ; Search time 2088 Seconds
(without alignments)
116.401 Million cell updates/sec

Title: US-09-335-032-71
Perfect score: 10
Sequence: 1 cttctctttt 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	10	100.0	25	29	CC457116	CC457116 SALK_1066
	2	10	100.0	28	9	AI686998	AI686998 tp81e01.x
	3	10	100.0	28	29	TA130B12P	AL464095 T. brucei
c	4	10	100.0	29	13	BQ590098	BQ590098 E012843-0
c	5	10	100.0	32	12	BI081179	BI081179 602879191
	6	10	100.0	32	29	AL941390	AL941390 Arabidops
	7	10	100.0	33	29	BZ763249	BZ763249 SALK_1157
c	8	10	100.0	34	9	AU256102	AU256102 AU256102
	9	10	100.0	37	28	AZ429862	AZ429862 1M0214I05
	10	10	100.0	37	28	AZ514585	AZ514585 1M0361B16
	11	10	100.0	39	28	AZ613373	AZ613373 1M0441M12
c	12	10	100.0	40	9	AA916182	AA916182 og34b06.s
c	13	10	100.0	41	28	AZ375959	AZ375959 1M0129A12
c	14	10	100.0	42	29	BX120830	BX120830 Danio rer
c	15	10	100.0	42	29	BX124544	BX124544 Danio rer
c	16	10	100.0	45	29	CC050354	CC050354 01S-536-6
c	17	10	100.0	45	29	BX120970	BX120970 Danio rer
	18	10	100.0	49	9	AA922976	AA922976 ok77e06.s
	19	10	100.0	49	9	AI564984	AI564984 tq53b02.x
	20	10	100.0	49	29	BZ357069	BZ357069 SALK_1301
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	22	10	100.0	51	29	BZ770334	BZ770334 SALK_1432
	23	10	100.0	51	29	AB082596	AB082596 Drosophil
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c	26	10	100.0	55	10	BE569086	BE569086 601339390
	27	10	100.0	55	28	BH908756	BH908756 SALK_0504
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	34	10	100.0	59	28	AZ774339	AZ774339 2M0003O05
	35	10	100.0	59	29	BZ354535	BZ354535 SALK_1252
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c	44	10	100.0	64	10	BE636308	BE636308 SWOvL2CAS
c	45	10	100.0	64	10	BE636320	BE636320 SWOvL2CAS
c	46	10	100.0	64	10	BE636344	BE636344 SWOvL2CAS
c	47	10	100.0	64	10	BE636363	BE636363 SWOvL2CAS
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c	63	10	100.0	65	28	AZ514453	AZ514453 1M0361N14
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c	67	10	100.0	65	29	AL949773	AL949773 Arabidops
c	68	10	100.0	65	29	TA129A12P	AL463978 T. brucei
c	69	10	100.0	66	14	W85242	W85242 mf52h08.r1
	70	10	100.0	66	28	AZ514401	AZ514401 1M0361K04
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	75	10	100.0	70	9	AL651716	AL651716 AL651716
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c	78	10	100.0	70	28	AZ918371 AZ918371 1006004B0
c	79	10	100.0	71	14	D78209 D78209 D78209 EST
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	82	10	100.0	72	29	BX285944 BX285944 Arabidops
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c	85	10	100.0	73	9	AW600116 AW600116 SWL4CAK10
c	86	10	100.0	73	9	AW626514 AW626514 SWOvL3CAN
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c	89	10	100.0	73	10	BG310475 BG310475 SWOv3MCAM
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c	92	10	100.0	73	10	BE420471 BE420471 SWOvL2CAS
c	93	10	100.0	73	10	BE420480 BE420480 SWOvL2CAS
c	94	10	100.0	73	10	BE638405 BE638405 SWOvL2CAS
c	95	10	100.0	73	10	BF228818 BF228818 SWOvL3CAN
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	99	10	100.0	75	29	TA77C02P AL460777 T. brucei
c	100	10	100.0	76	9	AA615345 AA615345 vo61d12.r
c	101	10	100.0	76	10	BF055674 BF055674 7i68d03.y
	102	10	100.0	76	28	AZ309821 AZ309821 1M0017C11
	103	10	100.0	76	29	AL768539 AL768539 Arabidops
	104	10	100.0	76	29	CNS02MOR AL204372 Tetraodon
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	106	10	100.0	77	14	CB099465 CB099465 ks10h09.y
	107	10	100.0	77	14	CB277589 CB277589 ks37d04.y
	108	10	100.0	77	14	CB277809 CB277809 ks39g02.y
	109	10	100.0	77	29	AL758789 AL758789 Arabidops
	110	10	100.0	78	29	AL762583 AL762583 Arabidops
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	113	10	100.0	81	28	BH855764 BH855764 SALK_0846
	114	10	100.0	82	28	BH911702 BH911702 SALK_0716
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c	116	10	100.0	83	10	BF507234 BF507234 4682P-15a
c	117	10	100.0	83	14	F14596 F14596 SSO4D05 Por
c	118	10	100.0	83	14	F37812 F37812 HSPD06839 H
	119	10	100.0	83	29	AL941379 AL941379 Arabidops
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	122	10	100.0	84	28	BH809934 BH809934 SALK_0367
	123	10	100.0	84	29	CNS041NL AL270426 Tetraodon
	124	10	100.0	85	12	BI703760 BI703760 kx18g12.y
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	126	10	100.0	85	14	U44279 U44279 ENU44279 As
c	127	10	100.0	85	28	AZ855489 AZ855489 2M0159L04
	128	10	100.0	85	28	BH862052 BH862052 SALK_0887
	129	10	100.0	85	29	BX288399 BX288399 Arabidops
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c	131	10	100.0	86	9	AJ547920 AJ547920 AJ547920
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c	133	10	100.0	86	29	BX175134 BX175134 Danio rer
	134	10	100.0	89	9	AV567495 AV567495 AV567495
c	135	10	100.0	89	28	BH251474 BH251474 SALK_0116
	136	10	100.0	89	29	BZ292893 BZ292893 SALK_1285
c	137	10	100.0	90	13	BQ098870 BQ098870 ph23b03.y
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	155	10	100.0	96	13	BU863237 BU863237 S025F09 P
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	157	10	100.0	96	29	BZ288800 BZ288800 SALK_0221
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c	189	10	100.0	103	12	BI127881 BI127881 G067P36Y
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	216	10	100.0	105	28	AZ797219 AZ797219 2M0053O15
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	219	10	100.0	106	9	AV902900 AV902900 AV902900
	220	10	100.0	106	10	BE840762 BE840762 MR2-SN000
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	226	10	100.0	107	14	H23901 H23901 yn75a05.r1
c	227	10	100.0	107	28	AZ565656 AZ565656 211PvF04
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	229	10	100.0	108	14	T83754 T83754 yd67h04.s1
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	231	10	100.0	108	28	BH416075 BH416075 1007046C0
c	232	10	100.0	109	9	AW753478 AW753478 PM0-CT026
	233	10	100.0	109	10	BE008587 BE008587 RC5-BN015
	234	10	100.0	109	10	BE012104 BE012104 RC5-BN105
c	235	10	100.0	109	10	BE315587 BE315587 NF023E10L
c	236	10	100.0	109	13	BQ591622 BQ591622 E012616-0
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	238	10	100.0	109	14	T91479 T91479 ye18h09.r1
	239	10	100.0	109	28	AQ080743 AQ080743 CIT-HSP-2
c	240	10	100.0	109	28	BH414927 BH414927 1007040E0
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	242	10	100.0	110	9	AV903734 AV903734 AV903734
	243	10	100.0	110	10	BG310551 BG310551 SWOv3MCAM
	244	10	100.0	110	14	CB006382 CB006382 VVC033B04
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	247	10	100.0	110	28	BH809571 BH809571 KG07049-3
	248	10	100.0	110	28	AQ385208 AQ385208 RPCI11-15
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	283	10	100.0	113	29	BZ358624 BZ358624 SALK_1330
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c	288	10	100.0	114	9	AW695613 AW695613 NF097A04S
	289	10	100.0	114	10	AW920975 AW920975 EST352279
	290	10	100.0	114	12	BJ538564 BJ538564 BJ538564
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	292	10	100.0	114	28	BH212127 BH212127 SALK_0071
	293	10	100.0	114	28	BH226094 BH226094 1006130A0
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	296	10	100.0	115	9	AV984486 AV984486 AV984486
	297	10	100.0	115	10	BF475908 BF475908 naa14c09.
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	306	10	100.0	116	28	BH078074 BH078074 RPCI-24-2
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	312	10	100.0	117	29	BZ764494 BZ764494 SALK_1250
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	315	10	100.0	118	9	AW481540 AW481540 36563 MAR
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	317	10	100.0	118	10	AW845662 AW845662 MR0-CT006
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	323	10	100.0	118	28	AZ247438 AZ247438 RPCI-23-3
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	334	10	100.0	119	28	BH542039 BH542039 BOGDH09TR
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	339	10	100.0	120	10	AW994767 AW994767 RC1-BN003
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	342	10	100.0	120	14	CD020233 CD020233 NXNV052A0
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	383	10	100.0	124	14	CB914818 CB914818 VVD097C04
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	394	10	100.0	126	12	BJ388788 BJ388788 BJ388788
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c	413	10	100.0	128	9	AV741497 AV741497 AV741497
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	425	10	100.0	130	10	BF084460 BF084460 RC2-CT052
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	482	10	100.0	136	10	BE080363 BE080363 QV1-BT063
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	497	10	100.0	137	12	BM484205 BM484205 537970 MA
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ALIGNMENTS

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RESULT 1
CC457116/c
LOCUS       CC457116                  25 bp    DNA     linear   GSS 30-MAY-2003
DEFINITION  SALK_106636.14.10.n Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_106636.14.10.n, genomic
            survey sequence.
ACCESSION   CC457116
VERSION     CC457116.1  GI:31218627
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
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  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_106636.14.10.n"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       16 a      1 c      7 g      1 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 2
AI686998
LOCUS       AI686998                 28 bp    mRNA    linear   EST 14-DEC-1999
DEFINITION  tp81e01.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2205720 3'
            similar to TR:O54875 O54875 MYOTONIC DYSTROPHY KINASE-RELATED
            CDC42-BINDING KINASE MRCK-BETA. ;contains element MER17 repetitive
            element ;, mRNA sequence.
ACCESSION   AI686998
VERSION     AI686998.1  GI:4898292
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center

            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2144   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2205720"
                     /tissue_type="poorly-differentiated endometrial
                     adenocarcinoma, 2 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut3"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.45 kb. Life Technologies catalog #:
                     11541-018"
BASE COUNT       4 a      12 c      0 g      12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          9 CTTCTCTTTT 18


RESULT 3
TA130B12P
LOCUS       TA130B12P                28 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 130b12, forward sequence,
            genomic survey sequence.
ACCESSION   AL464095
VERSION     AL464095.1  GI:11834358
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
```

```
                     /clone="130b12"
BASE COUNT        2 a      12 c       2 g      12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 28


RESULT 4
BQ590098/c
LOCUS       BQ590098                  29 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-O19-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-O19 3-PRIME, mRNA sequence.
ACCESSION   BQ590098
VERSION     BQ590098.1  GI:26119681
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 29   Std Error: 0.00
            Plate: 19  row: O  column: 19
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding line
                     )"
                     /db_xref="GABI:190019"
                     /db_xref="taxon:161934"
                     /clone="024-019-O19"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet project
                     , local PI: Dr. Katharina Schneider, coordinator: Prof.
                     Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
BASE COUNT       15 a      0 c      14 g      0 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 13;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 5
BI081179/c
LOCUS       BI081179                  32 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602879191F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010814 5',
            mRNA sequence.
ACCESSION   BI081179
VERSION     BI081179.1  GI:14499509
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11059  row: e  column: 23
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N-3"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5010814"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam2"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT       19 a      5 c      8 g      0 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 12;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 6
AL941390
LOCUS       AL941390                  32 bp    DNA     linear   GSS 24-OCT-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-257B04-014921,
            genomic survey sequence.
ACCESSION   AL941390
VERSION     AL941390.1  GI:24397988
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
```

```
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 32)
  AUTHORS   Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At5g42900. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-257B04-014921"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT        0 a      6 c      0 g     26 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 19


RESULT 7
BZ763249
LOCUS       BZ763249                  33 bp    DNA     linear   GSS 13-MAR-2003
DEFINITION  SALK_115724.25.30.n Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_115724.25.30.n, genomic
            survey sequence.
ACCESSION   BZ763249
VERSION     BZ763249.1  GI:28935802
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_115724.25.30.n"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT        9 a      7 c      3 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 19


RESULT 8
AU256102/c
LOCUS       AU256102                  34 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU256102 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0007468 3', mRNA sequence.
ACCESSION   AU256102
VERSION     AU256102.1  GI:20319468
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0007468"
                     /tissue_type="brain"
                     /clone_lib="3'-directed mouse cDNA library"
BASE COUNT       14 a      5 c      7 g      8 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 9
AZ429862
LOCUS       AZ429862                 37 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0214I05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0214I05 F, genomic survey sequence.
ACCESSION   AZ429862
VERSION     AZ429862.1  GI:10553875
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0214  row: I  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0214I05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        8 a      9 c      6 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 30


RESULT 10
AZ514585
LOCUS       AZ514585                 37 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0361B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0361B16 F, genomic survey sequence.
ACCESSION   AZ514585
VERSION     AZ514585.1  GI:10695817
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0361  row: B  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0361B16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        3 a      8 c      2 g     24 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 37;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
```

```
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 21


RESULT 11
AZ613373
LOCUS       AZ613373                 39 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0441M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0441M12 R, genomic survey sequence.
ACCESSION   AZ613373
VERSION     AZ613373.1  GI:11735563
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0441  row: M  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0441M12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        8 a      8 c      2 g     21 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          2 CTTCTCTTTT 11


RESULT 12
AA916182/c
LOCUS       AA916182                 40 bp    mRNA    linear   EST 14-APR-1998
DEFINITION  og34b06.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441715 3'
            similar to TR:Q33575 Q33575 NADH DEHYDROGENASE SUBUNIT 4. ;, mRNA
            sequence.
ACCESSION   AA916182
VERSION     AA916182.1  GI:3055574
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1441715"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Br7"
                     /note="Organ: breast; Vector: pCMV-SPORT4; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.2 kb. Life Technologies catalog
                     #:10985-018"
BASE COUNT       26 a      0 c     12 g      2 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 13
AZ375959/c
LOCUS       AZ375959                 41 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0129A12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0129A12 R, genomic survey sequence.
ACCESSION   AZ375959
VERSION     AZ375959.1  GI:10489659
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
```

```
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0129  row: A  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0129A12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       22 a      4 c      7 g      8 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 14
BX120830/c
LOCUS       BX120830                  42 bp    DNA     linear   GSS 13-MAR-2003
DEFINITION  Danio rerio genomic clone DKEY-61D1, genomic survey sequence.
ACCESSION   BX120830
VERSION     BX120830.1  GI:27951749
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 61D1. 61D1 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-61D1"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"
BASE COUNT       29 a      0 c     13 g      0 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         27 CTTCTCTTTT 18


RESULT 15
BX124544/c
LOCUS       BX124544                  42 bp    DNA     linear   GSS 28-JAN-2003
DEFINITION  Danio rerio genomic clone DKEY-64G19, genomic survey sequence.
ACCESSION   BX124544
VERSION     BX124544.1  GI:27955482
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 64G19. 64G19 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-64G19"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"
BASE COUNT       19 a      9 c      9 g      0 t      5 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 16
CC050354/c
LOCUS       CC050354                  45 bp    DNA     linear   GSS 01-APR-2003
DEFINITION  01S-536-6-1to6-G01 UniformMu MuTAIL Library Zea mays genomic clone
            01S-536-6-1to6-G01, genomic survey sequence.
```

```
ACCESSION   CC050354
VERSION     CC050354.1  GI:29465245
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
  TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
  JOURNAL   Unpublished
COMMENT     Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drm@ufl.edu
            Sequence flanking probable Mu insertion site in UniformMu line:
            01S-536-6
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="W22 (ACR, bz1-m9)"
                     /cultivar="UniformMu"
                     /db_xref="taxon:4577"
                     /clone="01S-536-6-1to6-G01"
                     /clone_lib="UniformMu MuTAIL Library"
                     /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                     insertions in Mu inactive lines were extracted from the
                     UniformMu maize population by the thermo assymmetric
                     interlaced PCR (TAIL) protocol using primers specific for
                     the Mu terminal inverted repeat and a set of 16 arbitrary
                     primers. Amplicons were size enriched using Sepharose 400
                     spin columns and cloned into the TOPO PCR4 vector."
BASE COUNT       17 a      6 c     16 g      6 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 29;  Length 45;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 17
BX120970/c
LOCUS       BX120970                 45 bp    DNA     linear   GSS 28-JAN-2003
DEFINITION  Danio rerio genomic clone DKEY-68A12, genomic survey sequence.
ACCESSION   BX120970
VERSION     BX120970.1  GI:27951891
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 68A12. 68A12 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-68A12"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"
BASE COUNT       28 a      2 c     15 g      0 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 29;  Length 45;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 18
AA922976
LOCUS       AA922976                 49 bp    mRNA    linear   EST 21-APR-1998
DEFINITION  ok77e06.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1520002 3'
            similar to TR:Q39614 Q39614 PROLINE-RICH PROTEIN. ;, mRNA sequence.
ACCESSION   AA922976
VERSION     AA922976.1  GI:3070285
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1520002"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GC4"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       10 a     23 c      0 g     16 t
ORIGIN

  Query Match           100.0%;  Score 10;  DB 9;  Length 49;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          1 CTTCTCTTTT 10


RESULT 19
AI564984
LOCUS       AI564984                 49 bp    mRNA    linear   EST 13-MAY-1999
DEFINITION  tq53b02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2212491 3'
            similar to WP:F59E12.9 CE11534 ;contains element MER22 repetitive
            element ;, mRNA sequence.
ACCESSION   AI564984
VERSION     AI564984.1  GI:4523441
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 400   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2212491"
                     /tissue_type="well-differentiated endometrial
                     adenocarcinoma, 7 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut1"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Life Technologies catalog #:
                     11538-014"
BASE COUNT        0 a     26 c      0 g     23 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          9 CTTCTCTTTT 18


RESULT 20
BZ357069
LOCUS       BZ357069                 49 bp    DNA     linear   GSS 14-NOV-2002
DEFINITION  SALK_130198.43.95.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_130198.43.95.x, genomic
            survey sequence.
ACCESSION   BZ357069
VERSION     BZ357069.1  GI:24948818
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_130198.43.95.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       12 a     13 c      5 g     19 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 21


RESULT 21
AU102691/c
LOCUS       AU102691                 50 bp    mRNA    linear   EST 30-AUG-2001
DEFINITION  AU102691 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HBMA230056, mRNA sequence.
ACCESSION   AU102691
VERSION     AU102691.1  GI:13552212
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
  JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
  MEDLINE   21270072
   PUBMED   11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
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          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: ysuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
          ,S. Construction and characterization of a full length-enriched and
          a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HBMA230056"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT       13 a     10 c     17 g     10 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         28 CTTCTCTTTT 19


RESULT 22
BZ770334
LOCUS       BZ770334                 51 bp    DNA     linear   GSS 13-MAR-2003
DEFINITION  SALK_143268.36.90.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_143268.36.90.x, genomic
            survey sequence.
ACCESSION   BZ770334
VERSION     BZ770334.1  GI:28944018
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_143268.36.90.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       14 a     10 c      5 g     22 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26


RESULT 23
AB082596
LOCUS       AB082596                 51 bp    DNA     linear   GSS 29-OCT-2002
DEFINITION  Drosophila melanogaster DNA, clone:l(2)SH2 1592, genomic survey
            sequence.
ACCESSION   AB082596
VERSION     AB082596.1  GI:24416782
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.
  TITLE     Fuctional Genomics: A P element-mediated gene disruption in
            Drosophila
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 51)
  AUTHORS   Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAR-2002) Suwan Oh, NCI-FCRDC, Lab. Of Immunobiology;
            1050 Boyles st., Frederick, Maryland 21702, USA
            (E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,
            Fax:1-301-846-6145)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="l(2)SH2 1592"
BASE COUNT        6 a     19 c      8 g     18 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         28 CTTCTCTTTT 37


RESULT 24
BQ667496/c
LOCUS       BQ667496                 52 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  pb62c12.y1 Anc caninum L3 serum stim pAMP1 v1 Chiapelli McCarter
            Ancylostoma caninum cDNA 5', mRNA sequence.
ACCESSION   BQ667496
VERSION     BQ667496.1  GI:21809178
KEYWORDS    EST.
SOURCE      Ancylostoma caninum (dog hookworm)
  ORGANISM  Ancylostoma caninum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
            Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
```

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  JOURNAL   Unpublished
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Brandi Chiapelli and Dr. James
            McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
            Washington University, St. Louis. DNA Sequencing by: Washington
            University Genome Sequencing Center St. Louis. Nematodes were
            provided by Dr. Prema Arasu of North Carolina State University.
            Putative full length read
            The vector to vector length is 53.
FEATURES              Location/Qualifiers
     source           1. .52
                      /organism="Ancylostoma caninum"
                      /mol_type="mRNA"
                      /db_xref="taxon:29170"
                      /dev_stage="serum stimulated L3"
                      /lab_host="DH10B"
                      /clone_lib="Anc caninum L3 serum stim pAMP1 v1 Chiapelli
                      McCarter"
                      /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                      The library was constructed by Brandi Chiapelli and Dr.
                      James  McCarter at Washington University, St. Louis.  The
                      cDNA was made by using Dynabead oligo-dT priming (Dynal).
                      PCR based library using a modified  protocol from the
                      SMART PCR cDNA Synthesis Kit from Clontech.  Directionally
                      cloned into the UDG sites of pAMP1.  Nematodes were
                      provided by Dr. Prema Arasu of North Carolina State
                      University."
BASE COUNT       32 a      3 c     13 g      4 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 13;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         44 CTTCTCTTTT 35


RESULT 25
AZ327146/c
LOCUS       AZ327146                 52 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M00050016F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M00050016 F, genomic survey sequence.
ACCESSION   AZ327146
VERSION     AZ327146.1  GI:10385604
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0050  row: O  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 52.
FEATURES              Location/Qualifiers
     source           1. .52
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0050016"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
BASE COUNT       26 a      7 c      9 g     10 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         32 CTTCTCTTTT 23


RESULT 26
BE569086/c
LOCUS       BE569086                 55 bp    mRNA    linear   EST 15-AUG-2000
DEFINITION  601339390F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681382 5',
            mRNA sequence.
ACCESSION   BE569086
VERSION     BE569086.1  GI:9812806
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM363  row: d  column: 23.
FEATURES              Location/Qualifiers
     source           1. .55
```

```
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3681382"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_53"
                     /note="Organ: bladder; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc
                     ); Double-stranded cDNA was prepared from cell line RNA.
                     5' and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T).   Average
                     insert size 1.55 kb (range 0.9-4.0 kb).  15/15 colonies
                     contained inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
BASE COUNT       40 a      1 c      11 g      3 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         48 CTTCTCTTTT 39


RESULT 27
BH908756
LOCUS       BH908756                 55 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_050419.22.05.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_050419.22.05.x, genomic
            survey sequence.
ACCESSION   BH908756
VERSION     BH908756.1  GI:22721689
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_050419.22.05.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       9 a      15 c      3 g      28 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         42 CTTCTCTTTT 51


RESULT 28
BH864698/c
LOCUS       BH864698                 56 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  SALK_096733 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_096733, genomic survey sequence.
ACCESSION   BH864698
VERSION     BH864698.1  GI:22100596
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_096733"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       19 a      5 c      12 g      20 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         53 CTTCTCTTTT 44


RESULT 29
BI322307
LOCUS       BI322307                 57 bp    mRNA    linear   EST 30-JUL-2001
```

```
DEFINITION  kx19c11.y3 Parastrongyloides trichosuri FL pAMP1 v1 Chiapelli
            McCarter Parastrongyloides trichosuri cDNA 5', mRNA sequence.
ACCESSION   BI322307
VERSION     BI322307.1  GI:15001493
KEYWORDS    EST.
SOURCE      Parastrongyloides trichosuri
  ORGANISM  Parastrongyloides trichosuri
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Panagrolaimoidea; Strongyloididae; Parastrongyloides.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Brandi Chiapelli and Dr. James
            McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
            Washington University, St. Louis. DNA Sequencing by: Washington
            University Genome Sequencing Center St. Louis.
            Putative full length read
            The vector to vector length is 58
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Parastrongyloides trichosuri"
                     /mol_type="mRNA"
                     /db_xref="taxon:131310"
                     /dev_stage="Free Living"
                     /lab_host="DH10B"
                     /clone_lib="Parastrongyloides trichosuri FL pAMP1 v1
                     Chiapelli McCarter"
                     /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                     The library was constructed by Brandi Chiapelli and Dr.
                     James McCarter at Washington University, St. Louis. The
                     cDNA was made by using Dynabead oligo-dT priming (Dynal).
                     PCR based library using a modified protocol from the
                     SMART PCR cDNA Synthesis Kit from Clontech. Directionally
                     cloned into the UDG sites of pAMP1. Nematodes were
                     provided by Dr. Warwick Grant of AgRearch, New Zealand
                     (warwick.grant@agresearch.co.nz)."
BASE COUNT       15 a      6 c      4 g     32 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 12;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 25


RESULT 30
CB917098/c
LOCUS       CB917098                 57 bp    mRNA    linear   EST 25-APR-2003
DEFINITION  VVD118G10_371857 An expressed sequence tag database for abiotic
            stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
            cDNA clone VVD118G10 5, mRNA sequence.
ACCESSION   CB917098
VERSION     CB917098.1  GI:30131759
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   Cushman,J.C.
  TITLE     An expressed sequence tag database for abiotic stressed berries of
            Vitis vinifera var. Chardonnay
  JOURNAL   Unpublished
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer (backward)
            Plate: 118  row: G  column: 10
            Seq primer: T3 20mer
            High quality sequence stop: 57.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /db_xref="taxon:29760"
                     /clone="VVD118G10"
                     /tissue_type="berries"
                     /dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
                     /clone_lib="An expressed sequence tag database for abiotic
                     stressed berries of Vitis vinifera var. Chardonnay"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
BASE COUNT       29 a      1 c     14 g     13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 14;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 31
AI343303/c
LOCUS       AI343303                 58 bp    mRNA    linear   EST 08-APR-1999
DEFINITION  tb92g09.x1 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2061856 3'
            similar to TR:Q33578 Q33578 KINETOPLAST CR5 ;, mRNA sequence.
ACCESSION   AI343303
VERSION     AI343303.1  GI:4080509
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
```

```
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .58
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2061856"
                      /tissue_type="bronchioalveolar carcinoma"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Lu25"
                      /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                      carcinoma tissue, cDNA made by oligo-dT  priming.
                      Directionally cloned.  Size-selected on agarose  gel,
                      average insert size 500 bp.  Primary library,
                      non-amplified.  "
BASE COUNT       34 a      15 c       8 g       1 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         47 CTTCTCTTTT 38


RESULT 32
BQ595228/c
LOCUS       BQ595228                 58 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012710-024-023-F23-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-023-F23 5-PRIME, mRNA sequence.
ACCESSION   BQ595228
VERSION     BQ595228.1  GI:26124811
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 58   Std Error: 0.00
            Plate: 23  row: F  column: 23
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .58
                      /organism="Beta vulgaris"
                      /mol_type="mRNA"
                      /cultivar="KWS2320 (double haploid, monogerm breeding line
                      )"
                      /db_xref="GABI:191621"
                      /db_xref="taxon:161934"
                      /clone="024-023-F23"
                      /tissue_type="developing root"
                      /lab_host="EMDH10B"
                      /clone_lib="MPIZ-ADIS-024-developing root"
                      /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet project
                      , local PI: Dr. Katharina Schneider, coordinator: Prof.
                      Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database: http://gabi.rzpd.de"
BASE COUNT       32 a       8 c      17 g       1 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 13;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         54 CTTCTCTTTT 45


RESULT 33
AU077187
LOCUS       AU077187                 59 bp    mRNA    linear   EST 04-MAY-2000
DEFINITION  AU077187 Sugano cDNA library Homo sapiens cDNA clone Zrv61646
            similar to 5'-end region of Mouse mRNA for proteasome Z subunit,
            mRNA sequence.
ACCESSION   AU077187
VERSION     AU077187.1  GI:7439801
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Suzuki,Y., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H., Tsunoda,T.
            , Watanabe,M., Komatsu,T., Ota,T., Isogai,T., Suyama,A. and Sugano
            ,S.
  TITLE     Statistical analysis of the 5' untranslated region of human mRNA
            using 'Oligo-Capped' cDNA libraries
  JOURNAL   Genomics 64 (3), 286-297 (2000)
  MEDLINE   20221373
   PUBMED   10756096
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997)
             This clone was obtained from a '5'-end-enriched' cDNA library
            constructed by 'Oligo-Capping' method. The coding region starts
            from the 50 bp upstream to the 3'-end.
FEATURES              Location/Qualifiers
     source           1. .59
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="Zrv61646"
                      /clone_lib="Sugano cDNA library"
BASE COUNT        9 a      12 c      19 g      19 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         48 CTTCTCTTTT 57


RESULT 34
AZ774339
```

```
LOCUS       AZ774339                 59 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0003O05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0003O05 R, genomic survey sequence.
ACCESSION   AZ774339
VERSION     AZ774339.1  GI:12899665
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0003  row: O  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 59.
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0003O05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       12 a      7 c     12 g     28 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 28


RESULT 35
BZ354535
LOCUS       BZ354535                 59 bp    DNA     linear   GSS 14-NOV-2002
DEFINITION  SALK_125268.25.05.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_125268.25.05.x, genomic
            survey sequence.
ACCESSION   BZ354535
VERSION     BZ354535.1  GI:24945397
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_125268.25.05.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       7 a     16 c     14 g     22 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          1 CTTCTCTTTT 10


RESULT 36
AL762585
LOCUS       AL762585                 59 bp    DNA     linear   GSS 19-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-026B10-013759,
            genomic survey sequence.
ACCESSION   AL762585
VERSION     AL762585.1  GI:21508841
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
```

(flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 59)
AUTHORS Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F23E13. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES Location/Qualifiers
source 1. .59
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-026B10-013759"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 9 a 11 c 12 g 27 t
ORIGIN

Query Match 100.0%; Score 10; DB 29; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 33 CTTCTCTTTT 42

RESULT 37
AU258677
LOCUS AU258677 63 bp mRNA linear EST 25-APR-2002
DEFINITION AU258677 3'-directed mouse cDNA library Mus musculus cDNA clone BED0013467 3', mRNA sequence.
ACCESSION AU258677
VERSION AU258677.1 GI:20324468
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 63)
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES Location/Qualifiers
source 1. .63
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0013467"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

BASE COUNT 16 a 11 c 11 g 24 t 1 others
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 15 CTTCTCTTTT 24

RESULT 38
AW874904/c
LOCUS AW874904 64 bp mRNA linear EST 22-MAY-2000
DEFINITION SWYACAL04A01SK Brugia malayi young adult cDNA (SAW99MLW-BmYA) Brugia malayi cDNA clone SWYACAL04A01 5', mRNA sequence.
ACCESSION AW874904
VERSION AW874904.1 GI:8012605
KEYWORDS EST.
SOURCE Brugia malayi
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in young adult of Brugia malayi
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.

FEATURES Location/Qualifiers
source 1. .64
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="SWYACAL04A01"
/dev_stage="young adult"
/lab_host="XL1-Blue MRF'"
/clone_lib="Brugia malayi young adult cDNA (SAW99MLW-BmYA)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.5 x 104 independent recombinants and the average insert size is approx. 800bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu."

BASE COUNT 25 a 10 c 18 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10

```
              ||||||||||
Db         34 CTTCTCTTTT 25


RESULT 39
AW874934/c
LOCUS       AW874934                 64 bp    mRNA    linear   EST 22-MAY-2000
DEFINITION  SWYACAL04D04SK Brugia malayi young adult cDNA (SAW99MLW-BmYA)
            Brugia malayi cDNA clone SWYACAL04D04 5', mRNA sequence.
ACCESSION   AW874934
VERSION     AW874934.1  GI:8012645
KEYWORDS    EST.
SOURCE      Brugia malayi
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in young adult of Brugia malayi
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Brugia malayi"
                     /mol_type="mRNA"
                     /db_xref="taxon:6279"
                     /clone="SWYACAL04D04"
                     /dev_stage="young adult"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Brugia malayi young adult cDNA (SAW99MLW-BmYA
                     )"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Lymphatic filarial nematode parasite of humans.
                     mRNA was prepared from young adult worms isolated from the
                     peritoneal cavity of jirds and converted to
                     double-stranded cDNA using reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The library
                     has 6.5 x 104 independent recombinants and the average
                     insert size is approx. 800bp.  The library was constructed
                     by Michelle Lizotte-Waniewski.  The library is available
                     from Dr. S.A. Williams,  email: genome@neal.smith.edu."
BASE COUNT       26 a     11 c     19 g      8 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 29


RESULT 40
BE239248/c
LOCUS       BE239248                 64 bp    mRNA    linear   EST 11-JUL-2000
DEFINITION  SWOvL2CAS08D03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS08D03 5', mRNA sequence.
ACCESSION   BE239248
VERSION     BE239248.1  GI:9034224
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS08D03"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       24 a      9 c     19 g     12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 41
BE239284/c
LOCUS       BE239284                 64 bp    mRNA    linear   EST 11-JUL-2000
DEFINITION  SWOvL2CAS08G03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS08G03 5', mRNA sequence.
ACCESSION   BE239284
VERSION     BE239284.1  GI:9034248
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
```

/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS08G03"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

BASE COUNT 25 a 9 c 19 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 14 CTTCTCTTTT 5

RESULT 42
BE239293/c
LOCUS BE239293 64 bp mRNA linear EST 11-JUL-2000
DEFINITION SWOvL2CAS08H03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) *Onchocerca volvulus* cDNA clone SWOvL2CAS08H03 5', mRNA sequence.
ACCESSION BE239293
VERSION BE239293.1 GI:9034257
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS08H03"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

BASE COUNT 29 a 11 c 15 g 9 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 47 CTTCTCTTTT 38

RESULT 43
BE636299/c
LOCUS BE636299 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvL2CAS13H10SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) *Onchocerca volvulus* cDNA clone SWOvL2CAS13H10 5', mRNA sequence.
ACCESSION BE636299
VERSION BE636299.1 GI:9919506
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS13H10"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

BASE COUNT 29 a 11 c 14 g 10 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 38 CTTCTCTTTT 29

RESULT 44
BE636308/c
LOCUS BE636308 64 bp mRNA linear EST 25-AUG-2000

```
DEFINITION  SWOvL2CAS14A09SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS14A09 5', mRNA sequence.
ACCESSION   BE636308
VERSION     BE636308.1  GI:9919515
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS14A09"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       23 a      9 c     19 g     13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 45
BE636320/c
LOCUS       BE636320                64 bp    mRNA    linear   EST 25-AUG-2000
DEFINITION  SWOvL2CAS14C02SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS14C02 5', mRNA sequence.
ACCESSION   BE636320
VERSION     BE636320.1  GI:9919527
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS14C02"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       26 a      8 c     19 g     11 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 46
BE636344/c
LOCUS       BE636344                64 bp    mRNA    linear   EST 25-AUG-2000
DEFINITION  SWOvL2CAS14E08SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS14E08 5', mRNA sequence.
ACCESSION   BE636344
VERSION     BE636344.1  GI:9919551
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS14E08"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
```

/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 30 a 10 c 14 g 10 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 38 CTTCTCTTTT 29

RESULT 47
BE636363/c
LOCUS BE636363 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvL2CAS14G07SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOvL2CAS14G07 5', mRNA sequence.
ACCESSION BE636363
VERSION BE636363.1 GI:9919570
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS14G07"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 27 a 8 c 18 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 18 CTTCTCTTTT 9

RESULT 48
BE636369/c
LOCUS BE636369 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvL2CAS14H03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOvL2CAS14H03 5', mRNA sequence.
ACCESSION BE636369
VERSION BE636369.1 GI:9919576
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS14H03"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 23 a 9 c 19 g 13 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 11 CTTCTCTTTT 2

RESULT 49
BE636392/c
LOCUS BE636392 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvAMCAQ09D08SK Onchocerca volvulus adult male cDNA (SAW98MLW-OvAM) Onchocerca volvulus cDNA clone SWOvAMCAQ09D08 5', mRNA sequence.
ACCESSION BE636392
VERSION BE636392.1 GI:9919419
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus

```
           Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
           Onchocercidae; Onchocerca.
REFERENCE  1  (bases 1 to 64)
  AUTHORS  Lizotte-Waniewski,M. and Williams,S.A.
  TITLE    Genes expressed in adult male stage of Onchocerca volvulus
  JOURNAL  Unpublished
COMMENT    Contact: Steven A. Williams
           Molecular Parasitology
           Smith College Department of Biological Sciences
           Department of Biological Sciences, Clark Science Center, Smith
           College, Northampton, MA, 01063, USA
           Tel: 4135853826
           Fax: 4135853786
           Email: genome@smith.edu
           Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvAMCAQ09D08"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus adult male cDNA
                     (SAW98MLW-OvAM)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. Six adult
                     male worms of Onchocerca  volvulus were isolated from
                     consenting patients and quick frozen.  Adult male mRNA was
                     converted to double-stranded cDNA using reverse
                     transcriptase and oligo(dT) followed by RNase H and DNA
                     pol I.  The library has 2 x 10E5 independent recombinants
                     and the average    insert size is ~1100bp.The library was
                     constructed by Michelle  Lizotte-Waniewski with worms
                     provided by Dr. Sara Lustigman. The library is  available
                     from Dr. Steven A. Williams, email: genome@smith.edu."
BASE COUNT       30 a     11 c     13 g     10 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         54 CTTCTCTTTT 45


RESULT 50
BE636430/c
LOCUS       BE636430                 64 bp    mRNA    linear   EST 25-AUG-2000
DEFINITION  SWOvL2CAS13C02SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS13C02 5', mRNA sequence.
ACCESSION   BE636430
VERSION     BE636430.1  GI:9919457
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS13C02"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       28 a      9 c     15 g     12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         33 CTTCTCTTTT 24


RESULT 51
BE636451/c
LOCUS       BE636451                 64 bp    mRNA    linear   EST 25-AUG-2000
DEFINITION  SWOvL2CAS13E09SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS13E09 5', mRNA sequence.
ACCESSION   BE636451
VERSION     BE636451.1  GI:9919478
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS13E09"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
```

oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 26 a 8 c 19 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 16 CTTCTCTTTT 7

RESULT 52
BE636456/c
LOCUS BE636456 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvL2CAS13F03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOvL2CAS13F03 5', mRNA sequence.
ACCESSION BE636456
VERSION BE636456.1 GI:9919483
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS13F03"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 29 a 13 c 13 g 9 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 41 CTTCTCTTTT 32

RESULT 53
BE636464/c
LOCUS BE636464 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvL2CAS13G02SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOvL2CAS13G02 5', mRNA sequence.
ACCESSION BE636464
VERSION BE636464.1 GI:9919491
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS13G02"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT 28 a 10 c 15 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 35 CTTCTCTTTT 26

RESULT 54
BE636472/c
LOCUS BE636472 64 bp mRNA linear EST 25-AUG-2000
DEFINITION SWOvL2CAS13H01SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOvL2CAS13H01 5', mRNA sequence.
ACCESSION BE636472
VERSION BE636472.1 GI:9919499
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus

```
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS13H01"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       26 a      7 c     19 g     12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 55
BF118488/c
LOCUS       BF118488                64 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  SWOvL3CAN69E12SK Onchocerca volvulus infective larva cDNA
            (SAW94WL-OvL3) Onchocerca volvulus cDNA clone SWOvL3CAN69E12 5',
            mRNA sequence.
ACCESSION   BF118488
VERSION     BF118488.1  GI:10992964
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A., Lu,W., Lizotte-Waniewski,M. and Laney,S.J.
  TITLE     Genes expressed in infective third stage larvae of Onchocerca
            volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Sierra Leone"
                     /db_xref="taxon:6282"
                     /clone="SWOvL3CAN69E12"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus infective larva cDNA
                     (SAW94WL-OvL3)"
                     /note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
                     Xho I; Cutaneous filarial nematode parasite of humans.
                     mRNA was prepared from third stage infective larvae of
                     Onchocerca volvulus isolated from mosquitoes 10 days after
                     infection and converted to double stranded cDNA using
                     reverse transcriptase and oligo(dT) followed by RNase H
                     and DNApol I. The library had 1.8 x 10E5 independent
                     recombinants and average insert size was 900 base pairs.
                     The library was constructed by Wenhong Lu. The library is
                     available from Dr. S.A. Williams, email genome@smith.edu."
BASE COUNT       27 a      8 c     18 g     11 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 56
BI097426/c
LOCUS       BI097426                64 bp    mRNA    linear   EST 25-JUN-2001
DEFINITION  SWOv3MCAM63F09SK Onchocerca volvulus molting L3 larva cDNA
            (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM63F09 5',
            mRNA sequence.
ACCESSION   BI097426
VERSION     BI097426.1  GI:14549083
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
  TITLE     Genes expressed in molting L3 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Kumba, Cameroons"
                     /db_xref="taxon:6282"
                     /clone="SWOv3MCAM63F09"
                     /dev_stage="molting L3"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus molting L3 larva cDNA
                     (SL96MLW-OvmL3)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. Third-stage
                     larvae, L3,  were isolated from infected black flies in
                     Cameroon (forest strain). The L3 were cultured in 20% FCS
                     in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
                     culture. L3 of O. volvulus molt to fourth-stage larvae by
                     day 5 in culture. mRNA was isolated from approximately
                     6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
```

in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

BASE COUNT 30 a 11 c 13 g 10 t
ORIGIN

Query Match 100.0%; Score 10; DB 12; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 40 CTTCTCTTTT 31

RESULT 57
BI142401/c
LOCUS BI142401 64 bp mRNA linear EST 05-JUL-2001
DEFINITION SWOv3MCAM62B04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62B04 5', mRNA sequence.
ACCESSION BI142401
VERSION BI142401.1 GI:14624111
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
TITLE Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM62B04"
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

BASE COUNT 27 a 10 c 15 g 12 t
ORIGIN

Query Match 100.0%; Score 10; DB 12; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 35 CTTCTCTTTT 26

RESULT 58
BI142408/c
LOCUS BI142408 64 bp mRNA linear EST 05-JUL-2001
DEFINITION SWOv3MCAM62B12SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62B12 5', mRNA sequence.
ACCESSION BI142408
VERSION BI142408.1 GI:14624118
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 64)
AUTHORS Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
TITLE Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .64
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM62B12"
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

BASE COUNT 28 a 8 c 17 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 12; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         30 CTTCTCTTTT 21


RESULT 59
BI142422/c
LOCUS       BI142422                64 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  SWOv3MCAM62D04SK Onchocerca volvulus molting L3 larva cDNA
            (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62D04 5',
            mRNA sequence.
ACCESSION   BI142422
VERSION     BI142422.1  GI:14624132
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
  TITLE     Genes expressed in molting L3 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Kumba, Cameroons"
                     /db_xref="taxon:6282"
                     /clone="SWOv3MCAM62D04"
                     /dev_stage="molting L3"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus molting L3 larva cDNA
                     (SL96MLW-OvmL3)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. Third-stage
                     larvae, L3,  were isolated from infected black flies in
                     Cameroon (forest strain). The L3 were cultured in 20% FCS
                     in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
                     culture. L3 of O. volvulus molt to fourth-stage larvae by
                     day 5 in culture. mRNA was isolated from approximately
                     6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                     in culture, and converted to double-stranded cDNA using
                     reverse transcriptase and oligo(dT) followed by RNase H
                     and DNA pol I. The library was constructed in the lambda
                     Uni-Zap XR vector and has 1 x 10E6 independent
                     recombinants and the average insert size is ~1200 bp. The
                     library was constructed by Sara Lustigman and Michelle
                     Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                     The library is available from Dr. Sara Lustigman (email:
                     slustigm@nybc.org)."
BASE COUNT       28 a      9 c     15 g     12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 12;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         34 CTTCTCTTTT 25


RESULT 60
BI142452/c
LOCUS       BI142452                64 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  SWOv3MCAM62F12SK Onchocerca volvulus molting L3 larva cDNA
            (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM62F12 5',
            mRNA sequence.
ACCESSION   BI142452
VERSION     BI142452.1  GI:14624162
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
  TITLE     Genes expressed in molting L3 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Kumba, Cameroons"
                     /db_xref="taxon:6282"
                     /clone="SWOv3MCAM62F12"
                     /dev_stage="molting L3"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus molting L3 larva cDNA
                     (SL96MLW-OvmL3)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. Third-stage
                     larvae, L3,  were isolated from infected black flies in
                     Cameroon (forest strain). The L3 were cultured in 20% FCS
                     in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
                     culture. L3 of O. volvulus molt to fourth-stage larvae by
                     day 5 in culture. mRNA was isolated from approximately
                     6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                     in culture, and converted to double-stranded cDNA using
                     reverse transcriptase and oligo(dT) followed by RNase H
                     and DNA pol I. The library was constructed in the lambda
                     Uni-Zap XR vector and has 1 x 10E6 independent
                     recombinants and the average insert size is ~1200 bp. The
                     library was constructed by Sara Lustigman and Michelle
                     Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                     The library is available from Dr. Sara Lustigman (email:
                     slustigm@nybc.org)."
BASE COUNT       27 a      10 c     15 g     12 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 12;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         35 CTTCTCTTTT 26


RESULT 61
AZ821452
LOCUS       AZ821452                64 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0094B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0094B14 F, genomic survey sequence.
ACCESSION   AZ821452
VERSION     AZ821452.1  GI:12991360
```

```
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0094  row: B  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 64.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0094B14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       14 a     12 c     12 g     26 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 25


RESULT 62
CB030041/c
LOCUS       CB030041                  65 bp    mRNA    linear   EST 13-JAN-2003
DEFINITION  TgESTzyd18e02.y1 TgRH Tachyzoite Norm 7 cDNA Library Toxoplasma
            gondii cDNA clone TgESTzyd18e02.y1 5', mRNA sequence.
ACCESSION   CB030041
VERSION     CB030041.1  GI:27726413
KEYWORDS    EST.
SOURCE      Toxoplasma gondii
  ORGANISM  Toxoplasma gondii
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Toxoplasma.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
            Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
            Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter
            ,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy
            ,S., Maguire,L., Waterston,R. and Wilson,R.
  TITLE     Toxoplasma EST Project
  JOURNAL   Unpublished
COMMENT     Contact: Clifton, S.
            Toxoplasma EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: toxo@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Seq primer: -40RP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Toxoplasma gondii"
                     /mol_type="mRNA"
                     /strain="RH (Type I)"
                     /db_xref="taxon:5811"
                     /clone="TgESTzyd18e02.y1"
                     /dev_stage="Tachyzoite"
                     /lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
                     /clone_lib="TgRH Tachyzoite Norm 7 cDNA Library"
                     /note="Vector: pBluscript SK-; Site_1: EcoRI; Site_2: XhoI
                     ; Toxoplasma RH strain tachyzoites were grown in human
                     foreskin fibroblast cultures in vitro. The library was
                     originally constructed by K.L.Wan, Cambridge University.
                     cDNAs were synthesized from polyA RNAs by oligo d(T)
                     priming and directionally cloned into the EcoRI to XhoI
                     sites of the Lambda ZapII vector using the ZAP-cDNA
                     synthesis kit (Stratagene). The primary cDNA library was
                     mass excised as phagemid using ExAssist helper phage
                     (Stratagene). Phagemid DNA was extracted by
                     phenol-chloroform method, and hybridized against a pool of
                     highly abundant genes which were derived from short-cycle
                     PCR of the primary cDNA library. The normalized library
                     was electroporated into DH10B (GeneHog, Invitrogen, Inc).
                     WARNING: the library contains a small percentage of cDNAs
                     derived from the human host cells."
BASE COUNT       31 a     7 c     20 g     7 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 14;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         58 CTTCTCTTTT 49


RESULT 63
AZ514453/c
LOCUS       AZ514453                  65 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0361N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0361N14 F, genomic survey sequence.
ACCESSION   AZ514453
VERSION     AZ514453.1  GI:10695865
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0361  row: N  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 65.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0361N14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       34 a      5 c     21 g      5 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 28;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 64
CC179177/c
LOCUS       CC179177                 65 bp    DNA     linear   GSS 02-MAY-2003
DEFINITION  SALK_059169.41.80.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_059169.41.80.x, genomic
            survey sequence.
ACCESSION   CC179177
VERSION     CC179177.1  GI:30317728
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At5g15860.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_059169.41.80.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       33 a      7 c     14 g     11 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         41 CTTCTCTTTT 32


RESULT 65
AG216203
LOCUS       AG216203                 65 bp    DNA     linear   GSS 03-SEP-2002
DEFINITION  Drosophila melanogaster DNA, clone:NP1611-5-1, flanking P{GaWB}
            transposon insertion, genomic survey sequence.
ACCESSION   AG216203
VERSION     AG216203.1  GI:22763203
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   Hayashi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H.,
            Aigaki,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R.,
            Uemura,T., Yoshihara,M. and Goto,S.
  TITLE     GETDB, a database compiling expression patterns and molecular
            locations of a collection of Gal4 enhancer traps
  JOURNAL   Genesis (2002) In press
REFERENCE   2  (bases 1 to 65)
  AUTHORS   Hayashi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
            Developmental Biology, Laboratory for Morphogenetic Singaling;
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            Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan
            (E-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
            Fax:81-78-301-3183)
COMMENT     This clone was isolated from genomic DNA flanking an insertion of
            the P element vector P{GaWB} of a Drosophila strain.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /strain="NP1611"
                     /db_xref="taxon:7227"
                     /chromosome="3"
                     /map="62E8"
                     /clone="NP1611-5-1"
                     /note="flanking P{GaWB} transposon insertion"
BASE COUNT        6 a      34 c       4 g      20 t       1 others
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         41 CTTCTCTTTT 50


RESULT 66
AL769814/c
LOCUS       AL769814                 65 bp    DNA     linear   GSS 19-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-092H08-012001,
            genomic survey sequence.
ACCESSION   AL769814
VERSION     AL769814.1  GI:21532016
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 65)
  AUTHORS   Rosso,M., Strizhov,N., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the right border of the T-DNA. It
            indicates an insertion within the locus defined by clone MGH6. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-092H08-012001"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT       32 a      9 c      11 g      13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         39 CTTCTCTTTT 30


RESULT 67
AL949773/c
LOCUS       AL949773                 65 bp    DNA     linear   GSS 24-OCT-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-323D01-015951,
            genomic survey sequence.
ACCESSION   AL949773
VERSION     AL949773.1  GI:24406395
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 65)
  AUTHORS   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion within the locus defined by clone F9H3. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-323D01-015951"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thalaina nuclear genome sequence were
                     processed for submission. T-DNA derived sequences were
```

removed"
BASE COUNT 26 a 7 c 17 g 15 t
ORIGIN

Query Match 100.0%; Score 10; DB 29; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 12 CTTCTCTTTT 3

RESULT 68
TA129A12P/c
LOCUS TA129A12P 65 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 129a12, forward sequence, genomic survey sequence.
ACCESSION AL463978
VERSION AL463978.1 GI:11834241
KEYWORDS GSS.
SOURCE *Trypanosoma brucei*
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 65)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .65
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="129a12"
BASE COUNT 31 a 7 c 22 g 5 t
ORIGIN

Query Match 100.0%; Score 10; DB 29; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 62 CTTCTCTTTT 53

RESULT 69
W85242/c
LOCUS W85242 66 bp mRNA linear EST 12-SEP-1996
DEFINITION mf52h08.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:408735 5' similar to gb:X13546_rna1 Human HMG-17 gene for non-histone chromosomal protein (HUMAN); gb:X12944 Mouse mRNA for HMG-17 chromosomal protein (MOUSE);, mRNA sequence.
ACCESSION W85242
VERSION W85242.1 GI:1397731
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 66)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:252503
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .66
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:408735"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
BASE COUNT 19 a 19 c 18 g 10 t
ORIGIN

Query Match 100.0%; Score 10; DB 14; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 41 CTTCTCTTTT 32

RESULT 70
AZ514401
LOCUS AZ514401 66 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0361K04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361K04 F, genomic survey sequence.
ACCESSION AZ514401
VERSION AZ514401.1 GI:10695717
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 66)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: K column: 04
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 66.
FEATURES Location/Qualifiers
source 1. .66
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361K04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 20 a 10 c 8 g 28 t
ORIGIN

Query Match 100.0%; Score 10; DB 28; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 17 CTTCTCTTTT 26

RESULT 71
AI442885
LOCUS AI442885 67 bp mRNA linear EST 28-NOV-2001
DEFINITION sa28b08.x1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1004-592 3' similar to TR:O24482 O24482 SALI3-2. ;, mRNA sequence.
ACCESSION AI442885
VERSION AI442885.1 GI:4299305
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 67)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
FEATURES Location/Qualifiers
source 1. .67
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1004-592"
/tissue_type="root"
/lab_host="XL10-Gold"
/clone_lib="Gm-c1004"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First- strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n=15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"
BASE COUNT 18 a 18 c 6 g 24 t 1 others
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;

```
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         56 CTTCTCTTTT 65


RESULT 72
CD029241
LOCUS       CD029241                67 bp    mRNA    linear   EST 07-MAY-2003
DEFINITION  mgns007xA10f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgns007xA10 5', mRNA sequence.
ACCESSION   CD029241
VERSION     CD029241.1  GI:30410697
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 67)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai
            ,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished
COMMENT     Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact person
            ;
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgns007  row: A  column: 10
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .67
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgns007xA10"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea NS Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI
                     ; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Nitrogen starvation library. Cells were inoculated into
                     minimal medium and grown for two days with shaking (150
                     rpm) at room temperature. Culture was harvested, blended,
                     inoculated into minimal medium as above for 24 h. Cells
                     were harvested, washed with water and inoculated into
                     minimal medium base lacking nitrogen source for 6 h.
                     Sequences were processed by one of two methods. Where a
                     full-length alignment to the M. grisea genome sequence was
                     available, the EST sequence was trimed according to the
                     alignment, otherwise sequence quality was assessed using
                     phredPhrap version 991019 and trimmed according to phd
                     files (0.05) and for vector seqs."
BASE COUNT       15 a     18 c     14 g     20 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 14;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 32


RESULT 73
BM447291/c
LOCUS       BM447291                68 bp    mRNA    linear   EST 01-APR-2002
DEFINITION  DSA008D10_57203 An expressed sequence tag database for the
            halotolerant green alga, Dunaliella salina Dunaliella salina cDNA
            clone DSA008D10 5, mRNA sequence.
ACCESSION   BM447291
VERSION     BM447291.1  GI:19852863
KEYWORDS    EST.
SOURCE      Dunaliella salina
  ORGANISM  Dunaliella salina
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Dunaliellaceae; Dunaliella.
REFERENCE   1  (bases 1 to 68)
  AUTHORS   Cushman,J.C.
  TITLE     An expressed sequence tag database for the halotolerant green alga,
            Dunaliella salina
  JOURNAL   Unpublished
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 008  row: D  column: 10
            Seq primer: T3 20mer
            High quality sequence stop: 68.
FEATURES             Location/Qualifiers
     source          1. .68
                     /organism="Dunaliella salina"
                     /mol_type="mRNA"
                     /db_xref="taxon:3046"
                     /clone="DSA008D10"
                     /tissue_type="Cells, which was adapted in 2.5M NaCl via a
                     incremental series from 1.7 to 2.0 to 2.25 to 2.5 M NaCl,
                     were exposed to 3.4 M NaCl for 5 hours"
                     /cell_type="Green"
                     /clone_lib="An expressed sequence tag database for the
                     halotolerant green alga, Dunaliella salina"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
BASE COUNT       22 a     13 c     24 g      9 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 12;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         42 CTTCTCTTTT 33


RESULT 74
AL757142/c
LOCUS       AL757142                68 bp    DNA     linear   GSS 18-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-118D11-012821,
            genomic survey sequence.
ACCESSION   AL757142
VERSION     AL757142.1  GI:21495490
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
JOURNAL Unpublished
REFERENCE 2
AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 68)
AUTHORS Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the right border of the T-DNA. It indicates an insertion within the locus defined by clone F27K19. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .68
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-118D11-012821"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
BASE COUNT 35 a 8 c 7 g 17 t 1 others
ORIGIN

Query Match 100.0%; Score 10; DB 29; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 53 CTTCTCTTTT 44

RESULT 75
AL651716
LOCUS AL651716 70 bp mRNA linear EST 13-DEC-2001
DEFINITION AL651716 XGC-gastrula Silurana tropicalis cDNA clone TGas036d16 5', mRNA sequence.
ACCESSION AL651716
VERSION AL651716.1 GI:17661928
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 70)
AUTHORS Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished
COMMENT Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas036d16.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
FEATURES Location/Qualifiers
source 1. .70
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas036d16"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 19 a 17 c 15 g 19 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 5 CTTCTCTTTT 14

RESULT 76
AA255635
LOCUS AA255635 70 bp mRNA linear EST 13-AUG-1997
DEFINITION zs31f07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686821 5' similar to SW:YKU2_YEAST P36042 HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-PAS1 INTERGENIC REGION. ;contains element TAR1 repetitive element ;, mRNA sequence.
ACCESSION AA255635
VERSION AA255635.1 GI:1892570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1914 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .70
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:686821"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 0 a 32 c 0 g 38 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 15 CTTCTCTTTT 24

RESULT 77
H45651/c
LOCUS H45651 70 bp mRNA linear EST 31-JUL-1995
DEFINITION yn97d02.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:176355 3' similar to gb|K01562|HUMCRHY1 Human Ro RNA (rRNA);, mRNA sequence.
ACCESSION H45651
VERSION H45651.1 GI:921703
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 979
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 979 Std Error: 0.00
Seq primer: SP6
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .70
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3838551"
/db_xref="taxon:9606"
/clone="IMAGE:176355"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55Y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

BASE COUNT 27 a 11 c 18 g 14 t
ORIGIN

Query Match 100.0%; Score 10; DB 14; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 13 CTTCTCTTTT 4

RESULT 78
AZ918371/c
LOCUS AZ918371 70 bp DNA linear GSS 17-DEC-2001
DEFINITION 1006004B08.x1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.
ACCESSION AZ918371
VERSION AZ918371.1 GI:13387655
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 70)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1006004 row: 36
Class: transposon-tagged.
FEATURES Location/Qualifiers
source 1. .70
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with ampicillin."
BASE COUNT 23 a 11 c 19 g 17 t
ORIGIN

Query Match 100.0%; Score 10; DB 28; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 44 CTTCTCTTTT 35

RESULT 79
D78209/c
LOCUS D78209 71 bp mRNA linear EST 23-MAR-1998
DEFINITION D78209 EST from 8p21.3-p22 Homo sapiens cDNA clone B6-1-5, mRNA sequence.
ACCESSION D78209
VERSION D78209.1 GI:2104127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 71)
AUTHORS Chinen,K., Isomura,M., Izawa,K., Fujiwara,Y., Ohata,H., Iwamasa,T. and Nakamura,Y.
TITLE Isolation of 45 exon-like fragments from 8p22-->p21.3, a region that is commonly deleted in hepatocellular, colorectal, and non-small cell lung carcinomas
JOURNAL Cytogenet. Cell Genet. 75 (2-3), 190-196 (1996)
MEDLINE 97193198
PUBMED 9040790
COMMENT Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
FEATURES Location/Qualifiers
source 1. .71
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="8p21.3-p22"
/clone="B6-1-5"
/clone_lib="EST from 8p21.3-p22"
BASE COUNT 29 a 8 c 21 g 13 t
ORIGIN

Query Match 100.0%; Score 10; DB 14; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 27 CTTCTCTTTT 18

RESULT 80
BZ770025/c
LOCUS BZ770025 71 bp DNA linear GSS 13-MAR-2003
DEFINITION SALK_142959.51.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_142959.51.10.x, genomic survey sequence.
ACCESSION BZ770025
VERSION BZ770025.1 GI:28943709
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 71)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P. , Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g01600.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .71
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_142959.51.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 28 a 13 c 8 g 22 t
ORIGIN

Query Match 100.0%; Score 10; DB 29; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 69 CTTCTCTTTT 60

RESULT 81
AA184862/c
LOCUS AA184862 72 bp mRNA linear EST 07-JAN-1997
DEFINITION mu51b11.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:642909 5' similar to gb:D13315 LACTOYLGLUTATHIONE LYASE (HUMAN);, mRNA sequence.
ACCESSION AA184862
VERSION AA184862.1 GI:1768508
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 72)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:394901
            Trace considered overall poor quality
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .72
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:642909"
                      /sex="male"
                      /tissue_type="lymph node"
                      /dev_stage="4 weeks"
                      /lab_host="DH10B"
                      /clone_lib="Soares mouse lymph node NbMLN"
                      /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
                      with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      1st strand cDNA was primed with a Not I - oligo(dT) primer
                      [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCGATACTTTTTTTTTTTTTTTTTTTTTT
                      3']; double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. RNA
                      provided by Dr. Bertrand Jordan. Library constructed and
                      normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT       28 a     13 c     17 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 82
BX285944
LOCUS       BX285944                72 bp    DNA     linear   GSS 07-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-386H01-018249,
            genomic survey sequence.
ACCESSION   BX285944
VERSION     BX285944.1  GI:28884940
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
            and Weisshaar,B.
  TITLE     A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
  TITLE     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 72)
  AUTHORS   Strizhov,N., Rosso,M., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At2g28150. The
            sequences are generated at the MPI for Plant Breeding Research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            Plant Genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES              Location/Qualifiers
     source           1. .72
                      /organism="Arabidopsis thaliana"
                      /mol_type="genomic DNA"
                      /strain="Columbia 0"
                      /db_xref="taxon:3702"
                      /clone="GK-386H01-018249"
                      /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                      /note="PCR was performed on DNA from Arabidopsis thaliana
                      plants (T1) which were transformed with the T-DNA from
                      vector pAC161. The lines contain one or more T-DNA
                      insertions. The DNA fragment(s) resulting from the PCR
                      were directly sequenced to determine the genomic sequence
                      flanking the insertion. Sequences displaying significant
                      similarity to the A. thalaina nuclear genome sequence were
                      processed for submission. T-DNA derived sequences were
                      removed"
BASE COUNT       11 a     11 c     16 g     34 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26


RESULT 83
AA262253/c
LOCUS       AA262253                73 bp    mRNA    linear   EST 06-AUG-1997
DEFINITION  zr70g04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:668790 5'
            similar to contains element PTR7 repetitive element ;, mRNA
            sequence.
ACCESSION   AA262253
VERSION     AA262253.1  GI:1898728
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1520   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 65.
FEATURES              Location/Qualifiers
     source           1. .73
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:668790"
                      /tissue_type="Pooled human melanocyte, fetal heart, and
                      pregnant uterus"
```

/lab_host="DH10B"
/clone_lib="Soares_NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 24 a 13 c 15 g 21 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 33 CTTCTCTTTT 24

RESULT 84
AW497651/c
LOCUS AW497651 73 bp mRNA linear EST 01-MAR-2000
DEFINITION SWYD25CAU11A07SK Brugia malayi young adult day 25 cDNA (SAW99MLW-BmYD25) Brugia malayi cDNA clone SWYD25CAU11A07 5', mRNA sequence.
ACCESSION AW497651
VERSION AW497651.1 GI:7119272
KEYWORDS EST.
SOURCE Brugia malayi
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 73)
AUTHORS Williams,S.A.
TITLE Genes expressed in young adult day 25 of Brugia malayi
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .73
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="SWYD25CAU11A07"
/dev_stage="young adult, twenty five days after infection"
/lab_host="XL1-Blue MRF'"
/clone_lib="Brugia malayi young adult day 25 cDNA (SAW99MLW-BmYD25)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds on day 25 after infection and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.2 x 105 independent recombinants and the average insert size is approx.1101bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu."
BASE COUNT 28 a 12 c 21 g 12 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 43 CTTCTCTTTT 34

RESULT 85
AW600116/c
LOCUS AW600116 73 bp mRNA linear EST 22-MAR-2000
DEFINITION SWL4CAK10B02SK Brugia malayi L4 cDNA (SAW99MLW-BmL4) Brugia malayi cDNA clone SWL4CAK10B02 5', mRNA sequence.
ACCESSION AW600116
VERSION AW600116.1 GI:7287629
KEYWORDS EST.
SOURCE Brugia malayi
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 73)
AUTHORS Williams,S.A.
TITLE Genes expressed in fourth stage larvae of Brugia malayi
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .73
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="SWL4CAK10B02"
/dev_stage="larval stage four"
/lab_host="XL1-Blue MRF'"
/clone_lib="Brugia malayi L4 cDNA (SAW99MLW-BmL4)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from L4s isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2.7 x 105 independent recombinants and the average insert size is approx. 1050bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email:genome@neal.smith.edu."
BASE COUNT 30 a 11 c 20 g 12 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 38 CTTCTCTTTT 29

RESULT 86
AW626514/c
LOCUS AW626514 73 bp mRNA linear EST 30-MAR-2000
DEFINITION SWOvL3CAN64C12SK Onchocerca volvulus infective larva cDNA (SAW94WL-OvL3) Onchocerca volvulus cDNA clone SWOvL3CAN64C12 5', mRNA sequence.

```
ACCESSION   AW626514
VERSION     AW626514.1  GI:7342379
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A., Lu,W., Lizotte-Waniewski,M. and Laney,S.J.
  TITLE     Genes expressed in infective third stage larvae of Onchocerca
            volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Sierra Leone"
                     /db_xref="taxon:6282"
                     /clone="SWOvL3CAN64C12"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus infective larva cDNA
                     (SAW94WL-OvL3)"
                     /note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
                     Xho I; Cutaneous filarial nematode parasite of humans.
                     mRNA was prepared from third stage infective larvae of
                     Onchocerca volvulus isolated from mosquitoes 10 days after
                     infection and converted to double stranded cDNA using
                     reverse transcriptase and oligo(dT) followed by RNase H
                     and DNApol I. The library had 1.8 x 10E5 independent
                     recombinants and average insert size was 900 base pairs.
                     The library was constructed by Wenhong Lu. The library is
                     available from Dr. S.A. Williams, email genome@smith.edu."
BASE COUNT       29 a      9 c     22 g     13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 87
AW626555/c
LOCUS       AW626555                  73 bp    mRNA    linear   EST 30-MAR-2000
DEFINITION  SWOvL3CAN66D01SK Onchocerca volvulus infective larva cDNA
            (SAW94WL-OvL3) Onchocerca volvulus cDNA clone SWOvL3CAN66D01 5',
            mRNA sequence.
ACCESSION   AW626555
VERSION     AW626555.1  GI:7342420
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A., Lu,W., Lizotte-Waniewski,M. and Laney,S.J.
  TITLE     Genes expressed in infective third stage larvae of Onchocerca
            volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Sierra Leone"
                     /db_xref="taxon:6282"
                     /clone="SWOvL3CAN66D01"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus infective larva cDNA
                     (SAW94WL-OvL3)"
                     /note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
                     Xho I; Cutaneous filarial nematode parasite of humans.
                     mRNA was prepared from third stage infective larvae of
                     Onchocerca volvulus isolated from mosquitoes 10 days after
                     infection and converted to double stranded cDNA using
                     reverse transcriptase and oligo(dT) followed by RNase H
                     and DNApol I. The library had 1.8 x 10E5 independent
                     recombinants and average insert size was 900 base pairs.
                     The library was constructed by Wenhong Lu. The library is
                     available from Dr. S.A. Williams, email genome@smith.edu."
BASE COUNT       26 a     11 c     21 g     15 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 9;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 88
AW651817/c
LOCUS       AW651817                  73 bp    mRNA    linear   EST 04-APR-2000
DEFINITION  SWYD25CAU14C02SK Brugia malayi young adult day 25 cDNA
            (SAW99MLW-BmYD25) Brugia malayi cDNA clone SWYD25CAU14C02 5', mRNA
            sequence.
ACCESSION   AW651817
VERSION     AW651817.1  GI:7413075
KEYWORDS    EST.
SOURCE      Brugia malayi
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in young adult day 25 of Brugia malayi
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Brugia malayi"
                     /mol_type="mRNA"
                     /db_xref="taxon:6279"
                     /clone="SWYD25CAU14C02"
                     /dev_stage="young adult, twenty five days after infection"
                     /lab_host="XL1-Blue MRF'"
```

/clone_lib="Brugia malayi young adult day 25 cDNA (SAW99MLW-BmYD25)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds on day 25 after infection and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.2 x 105 independent recombinants and the average insert size is approx.1101bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu."

BASE COUNT 29 a 11 c 22 g 11 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 38 CTTCTCTTTT 29

RESULT 89
BG310475/c
LOCUS BG310475 73 bp mRNA linear EST 23-FEB-2001
DEFINITION SWOv3MCAM55G11SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM55G11 5', mRNA sequence.
ACCESSION BG310475
VERSION BG310475.1 GI:13112333
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 73)
AUTHORS Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
TITLE Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .73
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM55G11"
/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

BASE COUNT 29 a 10 c 19 g 15 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 35 CTTCTCTTTT 26

RESULT 90
AW874933/c
LOCUS AW874933 73 bp mRNA linear EST 22-MAY-2000
DEFINITION SWYACAL04D03SK Brugia malayi young adult cDNA (SAW99MLW-BmYA) Brugia malayi cDNA clone SWYACAL04D03 5', mRNA sequence.
ACCESSION AW874933
VERSION AW874933.1 GI:8012644
KEYWORDS EST.
SOURCE Brugia malayi
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 73)
AUTHORS Williams,S.A.
TITLE Genes expressed in young adult of Brugia malayi
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .73
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="SWYACAL04D03"
/dev_stage="young adult"
/lab_host="XL1-Blue MRF'"
/clone_lib="Brugia malayi young adult cDNA (SAW99MLW-BmYA)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 6.5 x 104 independent recombinants and the average insert size is approx. 800bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu."

BASE COUNT 25 a 10 c 23 g 15 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 13 CTTCTCTTTT 4

```
RESULT 91
BE420470/c
LOCUS       BE420470                 73 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  SWOvL2CAS09D05SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS09D05 5', mRNA sequence.
ACCESSION   BE420470
VERSION     BE420470.1  GI:9418296
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS09D05"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       29 a     10 c     19 g     15 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         35 CTTCTCTTTT 26


RESULT 92
BE420471/c
LOCUS       BE420471                 73 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  SWOvL2CAS09D06SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS09D06 5', mRNA sequence.
ACCESSION   BE420471
VERSION     BE420471.1  GI:9418297
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
                     /clone="SWOvL2CAS09D06"
                     /dev_stage="L2"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus L2 larvae cDNA
                     (SAW98MLW-OvL2)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. mRNA was
                     prepared from approximately 9,000 L2s isolated from
                     infected  mosquitoes from Kumba, Cameroon and converted to
                     double-stranded cDNA using  reverse transcriptase and
                     oligo(dT) followed by RNase H and DNA pol I. The  library
                     has 7.3 x 10E4 independent recombinants and the average
                     insert size is  approximately 1kb.The library was
                     constructed by Michelle Lizotte-Waniewski.  The library is
                     available from Dr.S.A.Williams, email: genome@smith.edu."
BASE COUNT       29 a     10 c     21 g     13 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 10;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 93
BE420480/c
LOCUS       BE420480                 73 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  SWOvL2CAS09F04SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
            Onchocerca volvulus cDNA clone SWOvL2CAS09F04 5', mRNA sequence.
ACCESSION   BE420480
VERSION     BE420480.1  GI:9418306
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in L2 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6282"
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/clone="SWOvL2CAS09F04"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected *mosquitoes from* Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

BASE COUNT 31 a 12 c 16 g 14 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 41 CTTCTCTTTT 32

RESULT 94
BE638405/c
LOCUS BE638405 73 bp mRNA linear EST 28-AUG-2000
DEFINITION SWOvL2CAS15C01SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2) Onchocerca volvulus cDNA clone SWOvL2CAS15C01 5', mRNA sequence.
ACCESSION BE638405
VERSION BE638405.1 GI:9937024
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 73)
AUTHORS Williams,S.A.
TITLE Genes expressed in L2 larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .73
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvL2CAS15C01"
/dev_stage="L2"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10E4 independent recombinants and the average insert size is approximately 1kb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

BASE COUNT 29 a 11 c 19 g 13 t 1 others
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 27 CTTCTCTTTT 18

RESULT 95
BF228818/c
LOCUS BF228818 73 bp mRNA linear EST 13-NOV-2000
DEFINITION SWOvL3CAN76D10SK Onchocerca volvulus infective larva cDNA (SAW94WL-OvL3) Onchocerca volvulus cDNA clone SWOvL3CAN76D10 5', mRNA sequence.
ACCESSION BF228818
VERSION BF228818.1 GI:11141183
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 73)
AUTHORS Williams,S.A., Lu,W., Lizotte-Waniewski,M. and Laney,S.J.
TITLE Genes expressed in infective third stage larvae of Onchocerca volvulus
JOURNAL Unpublished
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .73
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Sierra Leone"
/db_xref="taxon:6282"
/clone="SWOvL3CAN76D10"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus infective larva cDNA (SAW94WL-OvL3)"
/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2: Xho I; Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu."

BASE COUNT 23 a 12 c 22 g 16 t
ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
||||||||||
Db 11 CTTCTCTTTT 2

RESULT 96
CB886667/c
LOCUS CB886667 73 bp mRNA linear EST 23-APR-2003

```
DEFINITION  SWOv3MCAM64D11SK Onchocerca volvulus molting L3 larva cDNA
            (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM64D11 5',
            mRNA sequence.
ACCESSION   CB886667
VERSION     CB886667.1  GI:30088462
KEYWORDS    EST.
SOURCE      Onchocerca volvulus
  ORGANISM  Onchocerca volvulus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Onchocerca.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A., Lizotte-Waniewski,M., Laney,S. and Lustigman,S.
  TITLE     Genes expressed in molting L3 larvae of Onchocerca volvulus
  JOURNAL   Unpublished
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Onchocerca volvulus"
                     /mol_type="mRNA"
                     /strain="Kumba, Cameroons"
                     /db_xref="taxon:6282"
                     /clone="SWOv3MCAM64D11"
                     /dev_stage="molting L3"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="Onchocerca volvulus molting L3 larva cDNA
                     (SL96MLW-OvmL3)"
                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                     Xho I; Filarial nematode parasite of humans. Third-stage
                     larvae, L3,  were isolated from infected black flies in
                     Cameroon (forest strain). The L3 were cultured in 20% FCS
                     in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
                     culture. L3 of O. volvulus molt to fourth-stage larvae by
                     day 5 in culture. mRNA was isolated from approximately
                     6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
                     in culture, and converted to double-stranded cDNA using
                     reverse transcriptase and oligo(dT) followed by RNase H
                     and DNA pol I. The library was constructed in the lambda
                     Uni-Zap XR vector and has 1 x 10E6 independent
                     recombinants and the average insert size is ~1200 bp. The
                     library was constructed by Sara Lustigman and Michelle
                     Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                     The library is available from Dr. Sara Lustigman (email:
                     slustigm@nybc.org)."
BASE COUNT       29 a     10 c     20 g     14 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 14;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         30 CTTCTCTTTT 21


RESULT 97
BZ660902
LOCUS       BZ660902                 74 bp    DNA     linear   GSS 31-JAN-2003
DEFINITION  SALK_024363.42.35.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_024363.42.35.x, genomic
            survey sequence.
ACCESSION   BZ660902
VERSION     BZ660902.1  GI:28174049
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At5g56780.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_024363.42.35.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT       15 a     14 c     23 g     22 t
ORIGIN

  Query Match             100.0%;  Score 10;  DB 29;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 30


RESULT 98
CA849383/c
LOCUS       CA849383                 75 bp    mRNA    linear   EST 16-DEC-2002
DEFINITION  kl11g03.y1 Ascaris suum embryo SL1 TOPO v1 Ascaris suum cDNA 5',
            mRNA sequence.
ACCESSION   CA849383
VERSION     CA849383.1  GI:27001294
KEYWORDS    EST.
SOURCE      Ascaris suum (pig roundworm)
  ORGANISM  Ascaris suum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea
            ; Ascarididae; Ascaris.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
```

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Embryo cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. 30-60 cell embryo material was provided by Dr. Richard Davis of City University of New York Graduate Center , College of Staten Island, Staten Island, NY (redavis@postbox.csi.cuny.edu).
Putative full length read
The vector to vector length is 82
Seq primer: SL1 primer.

FEATURES Location/Qualifiers
source 1. .75
/organism="Ascaris suum"
/mol_type="mRNA"
/db_xref="taxon:6253"
/dev_stage="30-60 cell embryo"
/lab_host="DH10B"
/clone_lib="Ascaris suum embryo SL1 TOPO v1"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI; Site_2: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Embryo cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. 30-60 cell embryo material was provided by Dr. Richard Davis of City University of New York Graduate Center, College of Staten Island, Staten Island, NY (redavis@postbox.csi.cuny.edu)."

BASE COUNT 34 a 10 c 14 g 17 t
ORIGIN

Query Match 100.0%; Score 10; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
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Db 58 CTTCTCTTTT 49

RESULT 99
TA77C02P
LOCUS TA77C02P 75 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 77c02, forward sequence, genomic survey sequence.
ACCESSION AL460777
VERSION AL460777.1 GI:11860526
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 75)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .75
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="77c02"

BASE COUNT 13 a 19 c 6 g 37 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
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Db 19 CTTCTCTTTT 28

RESULT 100
AA615345/c
LOCUS AA615345 76 bp mRNA linear EST 07-OCT-1997
DEFINITION vo61d12.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1054391 5' similar to SW:TRFE_RAT P12346 SEROTRANSFERRIN ;, mRNA sequence.
ACCESSION AA615345
VERSION AA615345.1 GI:2502573
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 76)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:585967
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1054391"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia

) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAATGGTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 22 a 17 c 21 g 16 t
ORIGIN

Query Match 100.0%; Score 10; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         34 CTTCTCTTTT 25
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Search completed: October 28, 2003, 18:19:28
Job time : 2140 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 28, 2003, 15:14:39 ; Search time 80 Seconds
(without alignments)
55.173 Million cell updates/sec

Title: US-09-335-032-71
Perfect score: 10
Sequence: 1 cttctctttt 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	10	100.0	12	2	US-08-173-489C-246	Sequence 246, App
	3	10	100.0	20	1	US-08-628-417-3	Sequence 3, Appli
c	4	10	100.0	20	4	US-09-198-452A-6382	Sequence 6382, Ap
c	5	10	100.0	21	2	US-08-229-528-16	Sequence 16, Appl
c	6	10	100.0	21	3	US-09-198-484-8	Sequence 8, Appli
	7	10	100.0	22	2	US-08-173-489C-65	Sequence 65, Appl
c	8	10	100.0	24	1	US-08-488-212A-17	Sequence 17, Appl
c	9	10	100.0	24	2	US-08-320-306-17	Sequence 17, Appl
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c	12	10	100.0	24	3	US-08-559-205-16	Sequence 16, Appl
c	13	10	100.0	24	4	US-09-417-722-3	Sequence 3, Appli
c	14	10	100.0	24	6	5336598-16	Patent No. 5336598
	15	10	100.0	25	1	US-08-628-417-4	Sequence 4, Appli
c	16	10	100.0	25	6	5217891-9	Patent No. 5217891
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c	18	10	100.0	27	4	US-08-584-040-7049	Sequence 7049, Ap
	19	10	100.0	29	4	US-09-270-542-133	Sequence 133, App
	20	10	100.0	30	4	US-09-270-542-132	Sequence 132, App
	21	10	100.0	30	4	US-09-270-542-134	Sequence 134, App
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	27	10	100.0	40	3	US-09-277-016-20	Sequence 20, Appl
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c	29	10	100.0	42	3	US-09-461-697-227	Sequence 227, App
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c	74	10	100.0	132	3	US-09-441-416A-22	Sequence 22, Appl
c	75	10	100.0	146	3	US-08-477-928A-36	Sequence 36, Appl
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c	78	10	100.0	189	3	US-09-461-697-213	Sequence 213, App
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c	86	10	100.0	228	4	US-09-016-434-99	Sequence 99, Appl
c	87	10	100.0	231	3	US-09-461-697-207	Sequence 207, App
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	92	10	100.0	241	4	US-09-620-405B-360	Sequence 360, App
	93	10	100.0	241	4	US-09-433-826B-360	Sequence 360, App
	94	10	100.0	241	4	US-09-604-287A-360	Sequence 360, App
c	95	10	100.0	247	4	US-09-016-434-737	Sequence 737, App
	96	10	100.0	251	3	US-09-098-789-9	Sequence 9, Appli
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c	100	10	100.0	267	4	US-09-134-001C-18	Sequence 18, Appl

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c 103	10	100.0	276	4	US-09-107-532A-1679	Sequence 1679, Ap
104	10	100.0	278	4	US-09-016-434-333	Sequence 333, App
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c 108	10	100.0	285	4	US-09-107-532A-598	Sequence 598, App
c 109	10	100.0	290	3	US-09-203-623-23	Sequence 23, Appl
c 110	10	100.0	290	4	US-09-313-294A-5996	Sequence 5996, Ap
c 111	10	100.0	290	4	US-09-523-462-23	Sequence 23, Appl
c 112	10	100.0	290	4	US-09-522-980-23	Sequence 23, Appl
c 113	10	100.0	294	4	US-09-328-352-310	Sequence 310, App
c 114	10	100.0	297	4	US-09-313-294A-7153	Sequence 7153, Ap
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c 116	10	100.0	300	4	US-09-313-294A-6323	Sequence 6323, Ap
117	10	100.0	306	3	US-09-172-108-19	Sequence 19, Appl
c 118	10	100.0	306	3	US-09-461-697-203	Sequence 203, App
c 119	10	100.0	309	4	US-09-313-294A-4076	Sequence 4076, Ap
c 120	10	100.0	312	4	US-09-107-532A-2593	Sequence 2593, Ap
c 121	10	100.0	315	3	US-08-617-860B-30	Sequence 30, Appl
c 122	10	100.0	316	4	US-09-702-705-1553	Sequence 1553, Ap
c 123	10	100.0	316	4	US-09-736-457-1553	Sequence 1553, Ap
c 124	10	100.0	318	4	US-09-107-532A-1431	Sequence 1431, Ap
125	10	100.0	318	4	US-09-107-532A-1846	Sequence 1846, Ap
c 126	10	100.0	320	3	US-09-030-607-224	Sequence 224, App
c 127	10	100.0	320	4	US-09-439-313-224	Sequence 224, App
c 128	10	100.0	320	4	US-09-352-616A-224	Sequence 224, App
c 129	10	100.0	320	4	US-09-232-149A-224	Sequence 224, App
c 130	10	100.0	335	3	US-09-018-584A-26	Sequence 26, Appl
c 131	10	100.0	335	4	US-09-199-542B-110	Sequence 110, App
c 132	10	100.0	337	4	US-09-589-287B-7	Sequence 7, Appli
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c 138	10	100.0	354	1	US-07-650-795A-2	Sequence 2, Appli
c 139	10	100.0	357	4	US-09-134-001C-19	Sequence 19, Appl
c 140	10	100.0	360	4	US-09-107-532A-2926	Sequence 2926, Ap
141	10	100.0	371	1	US-08-664-596B-25	Sequence 25, Appl
142	10	100.0	371	2	US-08-739-775-3	Sequence 3, Appli
c 143	10	100.0	372	1	US-08-474-633A-102	Sequence 102, App
c 144	10	100.0	372	4	US-08-823-771-102	Sequence 102, App
c 145	10	100.0	378	4	US-09-295-996B-3	Sequence 3, Appli
c 146	10	100.0	378	4	US-09-295-846B-3	Sequence 3, Appli
c 147	10	100.0	378	4	US-09-551-737C-3	Sequence 3, Appli
c 148	10	100.0	387	4	US-09-134-001C-253	Sequence 253, App
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c 150	10	100.0	393	4	US-09-107-532A-2668	Sequence 2668, Ap
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c 153	10	100.0	394	4	US-09-433-826B-448	Sequence 448, App
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c 155	10	100.0	401	4	US-09-643-597-299	Sequence 299, App
c 156	10	100.0	401	4	US-09-480-884A-299	Sequence 299, App
c 157	10	100.0	401	4	US-09-542-615A-299	Sequence 299, App
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161	10	100.0	414	1	US-08-592-126-98	Sequence 98, Appl
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c 163	10	100.0	420	3	US-08-991-890-1	Sequence 1, Appli
164	10	100.0	421	3	US-09-385-982-49	Sequence 49, Appl
165	10	100.0	434	4	US-09-280-116-31	Sequence 31, Appl
c 166	10	100.0	438	4	US-09-134-001C-2357	Sequence 2357, Ap
167	10	100.0	440	2	US-08-406-057-1	Sequence 1, Appli
168	10	100.0	440	3	US-08-958-316-1	Sequence 1, Appli
c 169	10	100.0	451	3	US-09-385-982-55	Sequence 55, Appl
c 170	10	100.0	452	4	US-09-221-017B-146	Sequence 146, App
171	10	100.0	456	4	US-09-227-357-110	Sequence 110, App
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173	10	100.0	460	4	US-09-120-561C-1	Sequence 1, Appli
174	10	100.0	465	6	5496550-9	Patent No. 5496550
175	10	100.0	466	6	5496550-7	Patent No. 5496550
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177	10	100.0	475	4	US-09-062-451-40	Sequence 40, Appl
c 178	10	100.0	475	4	US-09-004-838-5	Sequence 5, Appli
c 179	10	100.0	475	4	US-09-004-838-8	Sequence 8, Appli
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c 183	10	100.0	477	4	US-09-062-451-27	Sequence 27, Appl
c 184	10	100.0	477	4	US-09-598-326-27	Sequence 27, Appl
c 185	10	100.0	477	4	US-09-328-352-2089	Sequence 2089, Ap
c 186	10	100.0	477	4	US-09-289-198-27	Sequence 27, Appl
c 187	10	100.0	480	3	US-08-991-890-3	Sequence 3, Appli
c 188	10	100.0	484	4	US-09-702-705-645	Sequence 645, App
c 189	10	100.0	484	4	US-09-736-457-645	Sequence 645, App
c 190	10	100.0	486	1	US-08-828-511-1	Sequence 1, Appli
191	10	100.0	486	4	US-09-702-705-877	Sequence 877, App
192	10	100.0	486	4	US-09-736-457-877	Sequence 877, App
c 193	10	100.0	494	3	US-08-477-928A-35	Sequence 35, Appl
194	10	100.0	495	4	US-09-328-475C-209	Sequence 209, App
195	10	100.0	498	2	US-08-631-328-54	Sequence 54, Appl
c 196	10	100.0	498	6	5217891-7	Patent No. 5217891
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c 198	10	100.0	499	4	US-09-004-838-9	Sequence 9, Appli
199	10	100.0	499	4	US-09-328-475C-211	Sequence 211, App
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202	10	100.0	501	4	US-09-339-913B-98	Sequence 98, Appl
203	10	100.0	501	4	US-09-339-904A-87	Sequence 87, Appl
204	10	100.0	501	4	US-09-339-904A-93	Sequence 93, Appl
205	10	100.0	501	4	US-09-339-904A-98	Sequence 98, Appl
206	10	100.0	501	4	US-08-769-062B-87	Sequence 87, Appl
207	10	100.0	501	4	US-08-769-062B-93	Sequence 93, Appl
208	10	100.0	501	4	US-08-769-062B-98	Sequence 98, Appl
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210	10	100.0	501	4	US-09-344-002B-93	Sequence 93, Appl
211	10	100.0	501	4	US-09-344-002B-98	Sequence 98, Appl
212	10	100.0	501	4	US-09-559-565C-87	Sequence 87, Appl
213	10	100.0	501	4	US-09-559-565C-93	Sequence 93, Appl
214	10	100.0	501	4	US-09-559-565C-98	Sequence 98, Appl
215	10	100.0	501	4	US-09-693-350-87	Sequence 87, Appl
216	10	100.0	501	4	US-09-693-350-93	Sequence 93, Appl
217	10	100.0	501	4	US-09-693-350-98	Sequence 98, Appl
218	10	100.0	501	4	US-09-693-389-87	Sequence 87, Appl
219	10	100.0	501	4	US-09-693-389-93	Sequence 93, Appl
220	10	100.0	501	4	US-09-693-389-98	Sequence 98, Appl
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c 223	10	100.0	515	4	US-09-352-616A-472	Sequence 472, App
c 224	10	100.0	517	1	US-08-308-196A-14	Sequence 14, Appl
c 225	10	100.0	519	4	US-09-205-258-180	Sequence 180, App
226	10	100.0	521	4	US-09-404-879A-128	Sequence 128, App
227	10	100.0	521	4	US-09-338-933-128	Sequence 128, App
228	10	100.0	521	4	US-09-215-681-128	Sequence 128, App
c 229	10	100.0	531	4	US-08-671-548C-41	Sequence 41, Appl
c 230	10	100.0	531	4	US-08-671-548C-43	Sequence 43, Appl
c 231	10	100.0	532	4	US-09-679-409-48	Sequence 48, Appl
c 232	10	100.0	533	4	US-09-221-017B-216	Sequence 216, App
c 233	10	100.0	533	6	5482709-5	Patent No. 5482709
c 234	10	100.0	534	4	US-08-671-548C-13	Sequence 13, Appl
c 235	10	100.0	537	4	US-08-874-102-42	Sequence 42, Appl
236	10	100.0	537	4	US-08-874-102-43	Sequence 43, Appl
c 237	10	100.0	537	4	US-08-874-102-45	Sequence 45, Appl
c 238	10	100.0	537	4	US-08-984-919A-42	Sequence 42, Appl
239	10	100.0	537	4	US-08-984-919A-43	Sequence 43, Appl
c 240	10	100.0	537	4	US-08-984-919A-45	Sequence 45, Appl
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242	10	100.0	542	3	US-08-906-156A-65	Sequence 65, Appl
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c 245	10	100.0	544	4	US-09-004-838-137	Sequence 137, App
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c 251	10	100.0	578	3	US-08-991-789A-222	Sequence 222, App
c 252	10	100.0	578	4	US-09-062-451-222	Sequence 222, App
c 253	10	100.0	578	4	US-09-598-326-222	Sequence 222, App
c 254	10	100.0	578	4	US-09-289-198-222	Sequence 222, App
c 255	10	100.0	582	4	US-08-671-548C-39	Sequence 39, Appl
c 256	10	100.0	582	4	US-08-671-548C-45	Sequence 45, Appl
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258	10	100.0	591	4	US-09-702-705-1536	Sequence 1536, Ap
259	10	100.0	591	4	US-09-736-457-1332	Sequence 1332, Ap
260	10	100.0	591	4	US-09-736-457-1536	Sequence 1536, Ap
c 261	10	100.0	594	3	US-09-328-111-155	Sequence 155, App
262	10	100.0	599	3	US-09-385-982-446	Sequence 446, App
c 263	10	100.0	604	4	US-09-221-017B-1021	Sequence 1021, Ap
c 264	10	100.0	607	3	US-09-385-982-239	Sequence 239, App
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c 266	10	100.0	615	2	US-08-482-842B-3	Sequence 3, Appli
c 267	10	100.0	615	3	US-09-174-465D-1	Sequence 1, Appli
c 268	10	100.0	615	4	US-09-599-564A-1	Sequence 1, Appli
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270	10	100.0	621	3	US-09-328-111-602	Sequence 602, App
c 271	10	100.0	621	4	US-09-107-532A-2838	Sequence 2838, Ap
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273	10	100.0	628	4	US-09-227-357-104	Sequence 104, App
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277	10	100.0	642	4	US-09-736-457-77	Sequence 77, Appl
278	10	100.0	642	4	US-09-107-532A-1927	Sequence 1927, Ap
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c 280	10	100.0	648	4	US-08-961-527-376	Sequence 376, App
281	10	100.0	650	4	US-09-404-879A-262	Sequence 262, App
282	10	100.0	650	4	US-09-338-933-262	Sequence 262, App
283	10	100.0	650	4	US-09-215-681-262	Sequence 262, App
284	10	100.0	660	4	US-09-134-001C-2805	Sequence 2805, Ap
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c 286	10	100.0	669	4	US-09-669-751-79	Sequence 79, Appl
287	10	100.0	670	3	US-08-791-115B-13	Sequence 13, Appl
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c 290	10	100.0	678	4	US-09-107-532A-3648	Sequence 3648, Ap
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c 304	10	100.0	694	4	US-09-238-471-17	Sequence 17, Appl
c 305	10	100.0	696	3	US-09-461-697-193	Sequence 193, App
c 306	10	100.0	699	3	US-09-461-697-191	Sequence 191, App
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c 309	10	100.0	714	4	US-09-107-532A-3372	Sequence 3372, Ap
c 310	10	100.0	717	3	US-09-461-697-189	Sequence 189, App
c 311	10	100.0	718	3	US-08-998-416-961	Sequence 961, App
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315	10	100.0	720	3	US-09-299-843A-35	Sequence 35, Appl
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c 321	10	100.0	737	4	US-09-736-457-200	Sequence 200, App
c 322	10	100.0	740	2	US-08-739-775-5	Sequence 5, Appli
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326	10	100.0	773	4	US-09-227-357-47	Sequence 47, Appl
c 327	10	100.0	774	3	US-09-461-697-187	Sequence 187, App
328	10	100.0	776	4	US-09-535-008-37	Sequence 37, Appl
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c 330	10	100.0	783	1	US-08-446-922-5	Sequence 5, Appli
c 331	10	100.0	783	2	US-08-249-189-1	Sequence 1, Appli
c 332	10	100.0	783	2	US-08-484-624A-1	Sequence 1, Appli
c 333	10	100.0	783	2	US-08-477-733B-1	Sequence 1, Appli
c 334	10	100.0	783	3	US-09-088-913A-1	Sequence 1, Appli
c 335	10	100.0	783	3	US-08-769-819-1	Sequence 1, Appli
c 336	10	100.0	783	3	US-08-770-974-1	Sequence 1, Appli
c 337	10	100.0	783	4	US-08-770-981-1	Sequence 1, Appli
c 338	10	100.0	783	4	US-09-399-106-1	Sequence 1, Appli
c 339	10	100.0	783	5	PCT-US93-10034-5	Sequence 5, Appli
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341	10	100.0	791	4	US-09-659-845A-21	Sequence 21, Appl
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344	10	100.0	802	4	US-07-969-875A-18	Sequence 18, Appl
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c 347	10	100.0	813	4	US-09-107-532A-1790	Sequence 1790, Ap
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c 350	10	100.0	818	3	US-08-858-197-1	Sequence 1, Appli
c 351	10	100.0	819	3	US-09-461-697-185	Sequence 185, App
c 352	10	100.0	821	3	US-09-361-707-104	Sequence 104, App
353	10	100.0	825	4	US-09-280-116-225	Sequence 225, App
c 354	10	100.0	828	4	US-09-107-532A-1114	Sequence 1114, Ap
c 355	10	100.0	829	3	US-08-961-083-133	Sequence 133, App
c 356	10	100.0	829	4	US-09-556-877-56	Sequence 56, Appl
c 357	10	100.0	829	4	US-09-620-412C-56	Sequence 56, Appl
c 358	10	100.0	829	4	US-09-410-568-56	Sequence 56, Appl
c 359	10	100.0	829	4	US-09-598-419-56	Sequence 56, Appl
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363	10	100.0	846	4	US-09-328-352-325	Sequence 325, App
c 364	10	100.0	854	3	US-08-998-416-522	Sequence 522, App
c 365	10	100.0	855	4	US-09-565-423-1	Sequence 1, Appli
c 366	10	100.0	865	4	US-09-280-116-59	Sequence 59, Appl
367	10	100.0	872	3	US-08-943-731-130	Sequence 130, App
368	10	100.0	872	4	US-09-484-970B-147	Sequence 147, App
c 369	10	100.0	873	4	US-09-221-017B-251	Sequence 251, App
370	10	100.0	876	4	US-09-420-786A-2	Sequence 2, Appli
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c 373	10	100.0	878	2	US-08-477-733B-22	Sequence 22, Appl
c 374	10	100.0	878	3	US-09-088-913A-22	Sequence 22, Appl
c 375	10	100.0	878	3	US-08-769-819-22	Sequence 22, Appl
c 376	10	100.0	878	3	US-08-770-974-22	Sequence 22, Appl
c 377	10	100.0	878	4	US-08-770-981-22	Sequence 22, Appl
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c 381	10	100.0	903	4	US-09-589-287B-18	Sequence 18, Appl
c 382	10	100.0	903	4	US-09-588-947A-18	Sequence 18, Appl
c 383	10	100.0	906	4	US-09-134-001C-2072	Sequence 2072, Ap
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385	10	100.0	907	2	US-08-739-775-1	Sequence 1, Appli
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387	10	100.0	909	3	US-09-001-951-19	Sequence 19, Appl
388	10	100.0	909	4	US-08-818-829-19	Sequence 19, Appl
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c 390	10	100.0	927	4	US-09-328-352-1986	Sequence 1986, Ap
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c 392	10	100.0	930	4	US-09-107-532A-2737	Sequence 2737, Ap

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c 394	10	100.0	934	4	US-09-599-564A-4	Sequence 4, Appli
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396	10	100.0	951	4	US-09-556-877-118	Sequence 118, App
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398	10	100.0	951	4	US-09-598-419-118	Sequence 118, App
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c 403	10	100.0	957	2	US-08-445-533-7	Sequence 7, Appli
404	10	100.0	957	2	US-08-445-533-16	Sequence 16, Appl
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c 406	10	100.0	957	3	US-09-052-085-7	Sequence 7, Appli
407	10	100.0	957	3	US-09-052-085-16	Sequence 16, Appl
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413	10	100.0	984	3	US-08-748-506-9	Sequence 9, Appli
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c 418	10	100.0	1000	4	US-09-641-638-637	Sequence 637, App
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c 420	10	100.0	1001	4	US-09-641-638-169	Sequence 169, App
421	10	100.0	1001	4	US-09-641-638-555	Sequence 555, App
422	10	100.0	1001	4	US-09-671-317-174	Sequence 174, App
423	10	100.0	1001	4	US-09-671-317-272	Sequence 272, App
424	10	100.0	1001	4	US-09-671-317-273	Sequence 273, App
c 425	10	100.0	1001	4	US-09-671-317-309	Sequence 309, App
c 426	10	100.0	1001	4	US-09-671-317-333	Sequence 333, App
c 427	10	100.0	1001	4	US-09-671-317-334	Sequence 334, App
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429	10	100.0	1001	4	US-09-671-317-353	Sequence 353, App
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431	10	100.0	1001	4	US-09-671-317-402	Sequence 402, App
432	10	100.0	1001	4	US-09-671-317-453	Sequence 453, App
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c 435	10	100.0	1004	3	US-09-265-315-69	Sequence 69, Appl
c 436	10	100.0	1004	3	US-09-266-417-69	Sequence 69, Appl
c 437	10	100.0	1011	4	US-09-684-938-178	Sequence 178, App
c 438	10	100.0	1011	4	US-09-308-825A-178	Sequence 178, App
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443	10	100.0	1040	4	US-09-288-143-16	Sequence 16, Appl
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445	10	100.0	1046	3	US-08-333-576C-31	Sequence 31, Appl
446	10	100.0	1046	3	US-08-808-324-31	Sequence 31, Appl
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c 451	10	100.0	1082	2	US-08-453-051-3	Sequence 3, Appli
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c 453	10	100.0	1100	4	US-09-588-947A-1	Sequence 1, Appli
454	10	100.0	1101	4	US-08-984-919A-13	Sequence 13, Appl
c 455	10	100.0	1101	4	US-08-984-919A-14	Sequence 14, Appl
c 456	10	100.0	1105	3	US-08-837-317-1	Sequence 1, Appli
c 457	10	100.0	1105	4	US-09-573-885A-1	Sequence 1, Appli
458	10	100.0	1107	3	US-08-781-420-13	Sequence 13, Appl
c 459	10	100.0	1107	3	US-08-781-420-14	Sequence 14, Appl
460	10	100.0	1107	4	US-08-874-102-13	Sequence 13, Appl
c 461	10	100.0	1107	4	US-08-874-102-14	Sequence 14, Appl
462	10	100.0	1107	4	US-09-006-595A-13	Sequence 13, Appl
c 463	10	100.0	1107	4	US-09-006-595A-14	Sequence 14, Appl
464	10	100.0	1109	4	US-07-145-002B-31	Sequence 31, Appl
c 465	10	100.0	1113	4	US-09-107-532A-1614	Sequence 1614, Ap
466	10	100.0	1122	4	US-09-134-001C-1192	Sequence 1192, Ap
c 467	10	100.0	1124	2	US-08-966-316-11	Sequence 11, Appl
c 468	10	100.0	1125	4	US-09-134-001C-102	Sequence 102, App
469	10	100.0	1135	2	US-08-900-565-2	Sequence 2, Appli
470	10	100.0	1135	4	US-09-149-534-2	Sequence 2, Appli
471	10	100.0	1143	4	US-08-969-987-6	Sequence 6, Appli
c 472	10	100.0	1145	3	US-08-838-151A-19	Sequence 19, Appl
c 473	10	100.0	1145	3	US-08-838-151A-23	Sequence 23, Appl
c 474	10	100.0	1145	3	US-08-838-151A-26	Sequence 26, Appl
c 475	10	100.0	1145	3	US-08-838-151A-29	Sequence 29, Appl
c 476	10	100.0	1149	4	US-09-134-001C-610	Sequence 610, App
c 477	10	100.0	1154	2	US-08-369-829A-3	Sequence 3, Appli
c 478	10	100.0	1161	2	US-08-616-857-1	Sequence 1, Appli
479	10	100.0	1162	2	US-08-422-333-15	Sequence 15, Appl
480	10	100.0	1173	4	US-09-221-017B-1000	Sequence 1000, Ap
c 481	10	100.0	1173	4	US-09-107-532A-705	Sequence 705, App
c 482	10	100.0	1174	2	US-08-793-410-8	Sequence 8, Appli
483	10	100.0	1192	3	US-09-098-789-3	Sequence 3, Appli
c 484	10	100.0	1212	4	US-09-134-001C-2399	Sequence 2399, Ap
c 485	10	100.0	1218	4	US-09-286-981B-35	Sequence 35, Appl
486	10	100.0	1235	3	US-08-642-274D-36	Sequence 36, Appl
487	10	100.0	1235	3	US-08-952-014C-36	Sequence 36, Appl
c 488	10	100.0	1235	4	US-09-843-472-3	Sequence 3, Appli
c 489	10	100.0	1239	4	US-09-286-981B-22	Sequence 22, Appl
c 490	10	100.0	1246	4	US-09-302-769-22	Sequence 22, Appl
c 491	10	100.0	1258	4	US-09-286-981B-32	Sequence 32, Appl
c 492	10	100.0	1263	4	US-09-302-681-4	Sequence 4, Appli
493	10	100.0	1265	3	US-08-991-789A-169	Sequence 169, App
494	10	100.0	1265	4	US-09-062-451-169	Sequence 169, App
495	10	100.0	1265	4	US-09-598-326-169	Sequence 169, App
496	10	100.0	1265	4	US-09-289-198-169	Sequence 169, App
497	10	100.0	1272	4	US-09-206-344A-1	Sequence 1, Appli
c 498	10	100.0	1275	4	US-09-134-001C-1039	Sequence 1039, Ap
499	10	100.0	1275	4	US-09-328-352-2488	Sequence 2488, Ap
c 500	10	100.0	1279	4	US-09-620-312D-569	Sequence 569, App

ALIGNMENTS

```
RESULT 1
US-08-173-489C-181/c
; Sequence 181, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  181:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;      DESCRIPTION:  hepatitis B virus adw2 isolate,
;      DESCRIPTION:  nucleotides 807 to 818
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:
;      ORGANISM:  Hepatitis B virus
;      INDIVIDUAL ISOLATE:  adw2
;    PUBLICATION INFORMATION:
;      AUTHORS:  Valenzuela, P,  Quiroga, M,  Zaldivar, J,
;      AUTHORS:  Gray, P,  Ruter, W J.
;      TITLE:  The nucleotide sequence of
;      TITLE:  the Hepatitis B viral genome and the
;      TITLE:  identification of the major viral genes
;      JOURNAL:  In "Animal Virus Genetics", Fields, B N,
;      JOURNAL:  Jaenisch, R,  Fox C F eds
;      VOLUME:
;      PAGES:  57-70
;      DATE:  1980
;      RELEVANT RESIDUES IN SEQ ID NO:  181 :FROM 1 TO 12
US-08-173-489C-181

  Query Match             100.0%;  Score 10;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 2
US-08-173-489C-246
; Sequence 246, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  246:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  third strand derived from M. luteus
;      DESCRIPTION:  23s region in Seq ID No. 5861244245
;    HYPOTHETICAL:  yes
;    ANTI-SENSE:  no
;    PUBLICATION INFORMATION:
;      RELEVANT RESIDUES IN SEQ ID NO:  246 :FROM 1 TO 12
US-08-173-489C-246

  Query Match             100.0%;  Score 10;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          3 CTTCTCTTTT 12


RESULT 3
US-08-628-417-3
; Sequence 3, Application US/08628417
; Patent No. 5627054
;  GENERAL INFORMATION:
;    APPLICANT:  GILLESPIE, DAVID
;    TITLE OF INVENTION:  COMPETITOR PRIMER ASYMMETRIC
;    TITLE OF INVENTION:  POLYMERASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  U.S. ARMY CHEMICAL AND BIOLOGICAL
;      ADDRESSEE:  DEFENSE COMMAND
;      STREET:  OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
;      CITY:  ABERDEEN PROVING GROUND
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  21010-5423
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/628,417
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BIFFONI, ULYSSES J
;      REGISTRATION NUMBER:  39,908
;      REFERENCE/DOCKET NUMBER:  DAM 398-94
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  410-671-1158
;      TELEFAX:  410-671-2534
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligodeoxynucleotide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
;    ORIGINAL SOURCE:
;      ORGANISM:  Staphylococcus aureus
US-08-628-417-3
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  Query Match             100.0%;  Score 10;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 4
US-09-198-452A-6382/c
; Sequence 6382, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6382
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6382

  Query Match             100.0%;  Score 10;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 5
US-08-229-528-16/c
; Sequence 16, Application US/08229528
; Patent No. 5837447
;  GENERAL INFORMATION:
;    APPLICANT:  GORSKI, Jack
;    TITLE OF INVENTION:  MONITORING AN IMMUNE RESPONSE BY ANALYSIS OF AMPLIFIED IMMUNO
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  P. O. Box 1497
;      CITY:  Madison
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53701-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette,3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS 3.3
;      SOFTWARE:  WordPerfect, Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,528
;      FILING DATE:  18-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,569
;      FILING DATE:  15-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Scanlon, William J.
;      REGISTRATION NUMBER:  30,136
;      REFERENCE/DOCKET NUMBER:  30383/133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 258-4284
;      TELEFAX:  (608) 258-4258
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
US-08-229-528-16

  Query Match             100.0%;  Score 10;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 6
US-09-198-484-8/c
; Sequence 8, Application US/09198484
; Patent No. 6162435
; GENERAL INFORMATION:
;  APPLICANT: Minion, F. Chris
;  APPLICANT: Hsu, Tsungda
;  TITLE OF INVENTION: RECOMBINANT MYCOPLASMA HYOPNEUMONIAE VACCINE
;  FILE REFERENCE: I9000.028/P028
;  CURRENT APPLICATION NUMBER: US/09/198,484
;  CURRENT FILING DATE: 1998-11-24
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: primer
US-09-198-484-8

  Query Match             100.0%;  Score 10;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 7
US-08-173-489C-65
; Sequence 65, Application US/08173489C
; Patent No. 5861244
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, C. -G.
;    APPLICANT:  HEPBURN, A. G.
;    TITLE OF INVENTION:  GENETIC SEQUENCE ASSAY USING DNA
;    TITLE OF INVENTION:  TRIPLE-STRAND FORMATION.
;    NUMBER OF SEQUENCES:  365
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PROFILE DIAGNOSTIC SCIENCES, INC.,
;      STREET:  510 EAST 73RD STREET,
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10021.
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44Mb storage
;      COMPUTER:  IBM PC/XT/AT
;      OPERATING SYSTEM:  MS-DOS version 6.2
;      SOFTWARE:  Wordperfect Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,489C
;      FILING DATE:  22 DEC 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/968,436
;      FILING DATE:  29 OCT 1992
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Handelman, Joseph H.
;      REGISTRATION NUMBER:  26,179
;      REFERENCE/DOCKET NUMBER:  U9518-6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (attorney) (212) 708-1880
;      TELEFAX:  (attorney) (212) 246-8959
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  double stranded
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;      DESCRIPTION:  gamma-crystallin gene exon 3
;      DESCRIPTION:  (Accession # K03006) nucleotides 9 to 30
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  chromosome 2
;      MAP POSITION:  2q33-q35
;    PUBLICATION INFORMATION:
;      AUTHORS:  Meakin, S O,  Breitman, M L,  Tsui, L C.
;      TITLE:  Structural and evolutionary
;      TITLE:  relationships among five members of the human
;      TITLE:  gamma-crystallin gene family
;      JOURNAL:  Molecular and Cellular Biology
;      VOLUME:  5
;      PAGES:  1408-1414
;      DATE:  1985
;      RELEVANT RESIDUES IN SEQ ID NO:  65 :FROM 1 TO 22
US-08-173-489C-65

  Query Match             100.0%;  Score 10;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          6 CTTCTCTTTT 15


RESULT 8
US-08-488-212A-17/c
; Sequence 17, Application US/08488212A
; Patent No. 5665355
;  GENERAL INFORMATION:
;    APPLICANT:  Primi, Daniele
;    TITLE OF INVENTION:  Diagnosis and Treatment of
;    TITLE OF INVENTION:  AIDS Onset
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Thomas E. Popovich, Thomas
;      ADDRESSEE:  Popovich & Associates
;      STREET:  80 South 8th Street
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55402-2111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  Storage
;      COMPUTER:  IBM Compatible Compaq Prolinea
;      COMPUTER:  4/66
;      OPERATING SYSTEM:  MS-DOS Version 5
;      SOFTWARE:  Microsoft Word for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,212A
;      FILING DATE:  07-Jun-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,485
;      FILING DATE:  No. 5665355ember 9, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas E. Popovich
;      REGISTRATION NUMBER:  30099
;      REFERENCE/DOCKET NUMBER:  3678
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (612) 334-8991
;      TELEFAX:  (612) 334-8994
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 bases
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Other nucleic acid
;    MOLECULE TYPE:  (oligonucleotide useful in amplification of T Cell Receptor
;    MOLECULE TYPE:  Vb region)
;    HYPOTHETICAL:  No
;    ORIGINAL SOURCE:  Synthesized using
;    ORIGINAL SOURCE:  oligonucleotide synthesis machine
;    PUBLICATION INFORMATION:
;      AUTHORS:  Imberti, Luisa; Sottini,
;      AUTHORS:  Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
;      AUTHORS:  Daniele
;      TITLE:  Selective Depletion in HIV Infection
;      TITLE:  of T Cells That Bear Specific T Cell Receptor Vb Sequences
;      JOURNAL:  Science
;      VOLUME:  254
;      ISSUE:  5033
;      PAGES:  860-862
;      PUBLICATION DATE:  No. 5665355ember 8, 1991
US-08-488-212A-17

  Query Match             100.0%;  Score 10;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 9
US-08-320-306-17/c
; Sequence 17, Application US/08320306
; Patent No. 5891623
;  GENERAL INFORMATION:
;    APPLICANT:  Primi, Daniele
;    TITLE OF INVENTION:  Diagnosis and Treatment of
;    TITLE OF INVENTION:  AIDS Onset
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Thomas E. Popovich, Thomas
;      ADDRESSEE:  Popovich & Associates
;      STREET:  80 South 8th Street
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55402-2111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  Storage
;      COMPUTER:  IBM Compatible Compaq Prolinea
;      COMPUTER:  4/66
;      OPERATING SYSTEM:  MS-DOS Version 5
;      SOFTWARE:  Microsoft Word for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/320,306
;      FILING DATE:  06-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,485
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;       FILING DATE:  No. 5891623ember 9, 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Thomas E. Popovich
;       REGISTRATION NUMBER:  30099
;       REFERENCE/DOCKET NUMBER:  3678
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (612) 334-8991
;       TELEFAX:  (612) 334-8994
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 bases
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     MOLECULE TYPE:  Other nucleic acid
;     MOLECULE TYPE:  (oligonucleotide useful in amplification of T Cell Receptor
;     MOLECULE TYPE:  Vb region)
;     HYPOTHETICAL:  No
;     ORIGINAL SOURCE:  Synthesized using
;     ORIGINAL SOURCE:  oligonucleotide synthesis machine
;     PUBLICATION INFORMATION:
;       AUTHORS:  Imberti, Luisa; Sottini,
;       AUTHORS:  Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
;       AUTHORS:  Daniele
;       TITLE:  Selective Depletion in HIV Infection
;       TITLE:  of T Cells That Bear Specific T Cell Receptor Vb Sequences
;       JOURNAL:  Science
;       VOLUME:  254
;       ISSUE:  5033
;       PAGES:  860-862
;       PUBLICATION DATE:  No. 5891623ember 8, 1991
US-08-320-306-17

  Query Match             100.0%;  Score 10;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 10
US-08-488-209B-17/c
; Sequence 17, Application US/08488209B
; Patent No. 5925513
;  GENERAL INFORMATION:
;    APPLICANT:  Primi, Daniele
;    TITLE OF INVENTION:  Diagnosis and Treatment of
;    TITLE OF INVENTION:  AIDS Onset
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Thomas E. Popovich, Thomas
;      ADDRESSEE:  Popovich & Associates
;      STREET:  80 South 8th Street
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55402-2111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  Storage
;      COMPUTER:  IBM Compatible Compaq Prolinea
;      COMPUTER:  4/66
;      OPERATING SYSTEM:  MS-DOS Version 5
;      SOFTWARE:  Microsoft Word for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,209B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,485
;      FILING DATE:  No. 5925513ember 9, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Thomas E. Popovich
;      REGISTRATION NUMBER:  30099
;      REFERENCE/DOCKET NUMBER:  3678
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (612) 334-8991
;      TELEFAX:  (612) 334-8994
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 bases
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Other nucleic acid
;    MOLECULE TYPE:  (oligonucleotide useful in amplification of T Cell Receptor
;    MOLECULE TYPE:  Vb region)
;    HYPOTHETICAL:  No
;    ORIGINAL SOURCE:  Synthesized using
;    ORIGINAL SOURCE:  oligonucleotide synthesis machine
;    PUBLICATION INFORMATION:
;      AUTHORS:  Imberti, Luisa; Sottini,
;      AUTHORS:  Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
;      AUTHORS:  Daniele
;      TITLE:  Selective Depletion in HIV Infection
;      TITLE:  of T Cells That Bear Specific T Cell Receptor Vb Sequences
;      JOURNAL:  Science
;      VOLUME:  254
;      ISSUE:  5033
;      PAGES:  860-862
;      PUBLICATION DATE:  No. 5925513ember 8, 1991
US-08-488-209B-17

  Query Match             100.0%;  Score 10;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 11
US-08-408-011-17/c
; Sequence 17, Application US/08408011
; Patent No. 5928642
;  GENERAL INFORMATION:
;    APPLICANT:  Primi, Daniele
;    TITLE OF INVENTION:  Diagnosis and Treatment of
;    TITLE OF INVENTION:  AIDS Onset
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Thomas E. Popovich, Thomas
;      ADDRESSEE:  Popovich & Associates
;      STREET:  80 South 8th Street
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55402-2111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB
;      MEDIUM TYPE:  Storage
;      COMPUTER:  IBM Compatible Compaq Prolinea
;      COMPUTER:  4/66
;      OPERATING SYSTEM:  MS-DOS Version 5
;      SOFTWARE:  Microsoft Word for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/408,011
;      FILING DATE:  18-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,485
;      FILING DATE:  No. 5928642ember 9, 1992
;    ATTORNEY/AGENT INFORMATION:
```

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;       NAME:  Thomas E. Popovich
;       REGISTRATION NUMBER:  30099
;       REFERENCE/DOCKET NUMBER:  3678
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (612) 334-8991
;       TELEFAX:  (612) 334-8994
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  24 bases
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Single
;       TOPOLOGY:  Linear
;     MOLECULE TYPE:  Other nucleic acid
;     MOLECULE TYPE:  (oligonucleotide useful in amplification of T Cell Receptor
;     MOLECULE TYPE:  Vb region)
;     HYPOTHETICAL:  No
;     ORIGINAL SOURCE:  Synthesized using
;     ORIGINAL SOURCE:  oligonucleotide synthesis machine
;     PUBLICATION INFORMATION:
;       AUTHORS:  Imberti, Luisa; Sottini,
;       AUTHORS:  Alessandra; Bettinardi, Alessandra; Puoti, Massimo; Primi,
;       AUTHORS:  Daniele
;       TITLE:  Selective Depletion in HIV Infection
;       TITLE:  of T Cells That Bear Specific T Cell Receptor Vb Sequences
;       JOURNAL:  Science
;       VOLUME:  254
;       ISSUE:  5033
;       PAGES:  860-862
;       PUBLICATION DATE:  No. 5928642ember 8, 1991
US-08-408-011-17

  Query Match             100.0%;  Score 10;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 12
US-08-559-205-16/c
; Sequence 16, Application US/08559205
; Patent No. 6087096
;  GENERAL INFORMATION:
;    APPLICANT:  Dau, Peter C.
;    APPLICANT:  Liu, Debang
;    TITLE OF INVENTION:  Method of Intrafamily Fragment Analysis of the T
;    TITLE OF INVENTION:  Cell Receptor ' and   Chain CDR3 Regions
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,205
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gass, David A.
;      REGISTRATION NUMBER:  38,153
;      REFERENCE/DOCKET NUMBER:  28721/32972
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-559-205-16

  Query Match             100.0%;  Score 10;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 13
US-09-417-722-3/c
; Sequence 3, Application US/09417722
; Patent No. 6309837
; GENERAL INFORMATION:
;  APPLICANT: Dean, Ralph A.
;  APPLICANT: Wang, Yi-Hong
;  TITLE OF INVENTION: PCR-based Method for Identifying a Fusarium
;  TITLE OF INVENTION: Wilt-Resistant Genotype in Plants
;  FILE REFERENCE: PCR ID: Fusarium-resistant genotype
;  CURRENT APPLICATION NUMBER: US/09/417,722
;  CURRENT FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: forward PCR
;   OTHER INFORMATION: primer of FM primer pair
US-09-417-722-3

  Query Match             100.0%;  Score 10;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 14
5336598-16/c
;Patent No. 5336598
;    APPLICANT: KOTZIN, BRIAN L.;MARRACK, PHILIPPA;KAPPLER,
;JOHN;CHOI, YOUNGWON
;    TITLE OF INVENTION: METHOD FOR DIAGNOSING A SUPERANTIGEN
;CAUSED PATHOLOGIAL CONDITION VIA ASSAY OF T-CELLS
;    NUMBER OF SEQUENCES: 25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/437,370
;      FILING DATE: 15-NOV-1989
;SEQ ID NO:16:
;      LENGTH: 24
5336598-16

  Query Match             100.0%;  Score 10;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9
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RESULT 15
US-08-628-417-4
; Sequence 4, Application US/08628417
; Patent No. 5627054
;  GENERAL INFORMATION:
;    APPLICANT:  GILLESPIE, DAVID
;    TITLE OF INVENTION:  COMPETITOR PRIMER ASYMMETRIC
;    TITLE OF INVENTION:  POLYMERASE CHAIN REACTION
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  U.S. ARMY CHEMICAL AND BIOLOGICAL
;      ADDRESSEE:  DEFENSE COMMAND
;      STREET:  OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
;      CITY:  ABERDEEN PROVING GROUND
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  21010-5423
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/628,417
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BIFFONI, ULYSSES J
;      REGISTRATION NUMBER:  39,908
;      REFERENCE/DOCKET NUMBER:  DAM 398-94
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  410-671-1158
;      TELEFAX:  410-671-2534
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligodeoxynucleotide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  YES
US-08-628-417-4

  Query Match            100.0%;  Score 10;  DB 1;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 16
5217891-9/c
;Patent No. 5217891
;    APPLICANT: BRAKE, ANTHONY J.;VAN DEN BERG, JOHAN A.
;    TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
;A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
;POLYPEPTIDES
;    NUMBER OF SEQUENCES: 23
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/507,398
;      FILING DATE: 09-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 78,551
;      FILING DATE: 28-JUL-1987
;SEQ ID NO:9:
;      LENGTH: 25
5217891-9

  Query Match            100.0%;  Score 10;  DB 6;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 17
US-08-412-376-23/c
; Sequence 23, Application US/08412376
; Patent No. 5849900
;  GENERAL INFORMATION:
;    APPLICANT:  Moelling, Karin
;    TITLE OF INVENTION:  Inhibition Of Viruses By Antisense
;    TITLE OF INVENTION:  Oligomers Capable Of Binding To Polypurine-Rich Tract Of Sin
;    TITLE OF INVENTION:  Stranded RNA Or RNA-DNA Hybrids
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz
;      ADDRESSEE:  Mackiewicz & No. 5849900ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/412,376
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/954,184
;      FILING DATE:  29-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Doreen Yatko Trujillo
;      REGISTRATION NUMBER:  35,719
;      REFERENCE/DOCKET NUMBER:  APOL-0021
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  Yes
US-08-412-376-23

  Query Match            100.0%;  Score 10;  DB 2;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 18
US-08-584-040-7049/c
; Sequence 7049, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
```

```
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7049:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      OTHER INFORMATION:  The letter "N" represents the stem II region
;      OTHER INFORMATION:  of an HH ribozyme.
US-08-584-040-7049

  Query Match             100.0%;  Score 10;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         27 CTTCTCTTTT 18


RESULT 19
US-09-270-542-133
; Sequence 133, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
;  APPLICANT: Aitman, Timothy
;  APPLICANT: Scott, James
;  APPLICANT: Stanton, Lawrence
;  TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: 4198/78179
;  CURRENT APPLICATION NUMBER: US/09/270,542
;  CURRENT FILING DATE: 1999-03-17
;  EARLIER APPLICATION NUMBER: 09/221,222
;  EARLIER FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-270-542-133

  Query Match             100.0%;  Score 10;  DB 4;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 20
US-09-270-542-132
; Sequence 132, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
;  APPLICANT: Aitman, Timothy
;  APPLICANT: Scott, James
;  APPLICANT: Stanton, Lawrence
;  TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: 4198/78179
;  CURRENT APPLICATION NUMBER: US/09/270,542
;  CURRENT FILING DATE: 1999-03-17
;  EARLIER APPLICATION NUMBER: 09/221,222
;  EARLIER FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-270-542-132

  Query Match             100.0%;  Score 10;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 21
US-09-270-542-134
; Sequence 134, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
;  APPLICANT: Aitman, Timothy
;  APPLICANT: Scott, James
;  APPLICANT: Stanton, Lawrence
;  TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: 4198/78179
;  CURRENT APPLICATION NUMBER: US/09/270,542
;  CURRENT FILING DATE: 1999-03-17
;  EARLIER APPLICATION NUMBER: 09/221,222
;  EARLIER FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-270-542-134

  Query Match             100.0%;  Score 10;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 22
US-09-270-542-135
; Sequence 135, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
;  APPLICANT: Aitman, Timothy
;  APPLICANT: Scott, James
;  APPLICANT: Stanton, Lawrence
;  TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: 4198/78179
;  CURRENT APPLICATION NUMBER: US/09/270,542
;  CURRENT FILING DATE: 1999-03-17
;  EARLIER APPLICATION NUMBER: 09/221,222
;  EARLIER FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-270-542-135

  Query Match             100.0%;  Score 10;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          8 CTTCTCTTTT 17


RESULT 23
US-08-961-083-359/c
; Sequence 359, Application US/08961083
; Patent No. 6159469
;  GENERAL INFORMATION:
;    APPLICANT:  Choi et. al.
;    TITLE OF INVENTION:  Streptococcus pneumoniae Antigens and Vaccines
;    NUMBER OF SEQUENCES:  452
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,083
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  359:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-961-083-359

  Query Match             100.0%;  Score 10;  DB 3;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 24
US-09-536-784-359/c
; Sequence 359, Application US/09536784
; Patent No. 6573082
;   GENERAL INFORMATION:
;        APPLICANT: Choi et. al.
;        TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
;        NUMBER OF SEQUENCES: 452
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/536,784
;             FILING DATE: 30-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/961,083
;             FILING DATE: OCT-30-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Michelle S. Marks
;             REGISTRATION NUMBER: 41,971
;             REFERENCE/DOCKET NUMBER: PB340P3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (301) 309-8504
;             TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 359:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 33 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 359:
US-09-536-784-359

  Query Match             100.0%;  Score 10;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 25
US-09-371-772B-10906/c
; Sequence 10906, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
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;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10906
;    LENGTH: 38
;    TYPE: RNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-371-772B-10906

  Query Match             100.0%;  Score 10;  DB 4;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 29


RESULT 26
5217891-13/c
;Patent No. 5217891
;    APPLICANT: BRAKE, ANTHONY J.;VAN DEN BERG, JOHAN A.
;    TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
;A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
;POLYPEPTIDES
;    NUMBER OF SEQUENCES: 23
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/507,398
;      FILING DATE: 09-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 78,551
;      FILING DATE: 28-JUL-1987
;SEQ ID NO:13:
;      LENGTH: 39
5217891-13

  Query Match             100.0%;  Score 10;  DB 6;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 27
US-09-277-016-20
; Sequence 20, Application US/09277016
; Patent No. 6143529
; GENERAL INFORMATION:
;  APPLICANT: Lapidus, Stanley N
;  APPLICANT: Shuber, Anthony P
;  TITLE OF INVENTION: Methods for improving sensitivity and specificity of
;  TITLE OF INVENTION: screening assays
;  FILE REFERENCE: EXT-030
;  CURRENT APPLICATION NUMBER: US/09/277,016
;  CURRENT FILING DATE: 1999-03-26
;  EARLIER APPLICATION NUMBER: 08/876,857
;  EARLIER FILING DATE: 1997-06-16
;  EARLIER APPLICATION NUMBER: 08/700,583
;  EARLIER FILING DATE: 1996-08-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;    LENGTH: 40
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:PCR-G-FOR (p53
;    OTHER INFORMATION: Exon 8)
US-09-277-016-20

  Query Match             100.0%;  Score 10;  DB 3;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         31 CTTCTCTTTT 40


RESULT 28
US-07-908-317-33
; Sequence 33, Application US/07908317
; Patent No. 5420027
;  GENERAL INFORMATION:
;    APPLICANT:  FISHER, CHARLES W.
;    APPLICANT:  BARNES, HENRY J.
;    APPLICANT:  ESTABROOK, RONALD W.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  THE EXPRESSION OF BILOGICALLY
;    TITLE OF INVENTION:  ACTIVE FUSION PROTEINS COMPRISING A
;    TITLE OF INVENTION:  EUKARYOTIC CYTOCHROME P450 FUSED TO
;    TITLE OF INVENTION:  A REDUCTASE IN BACTERIA
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/908,317
;      FILING DATE:  19920702
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARKER, DAVID L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTSD:292/PAR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512-320-7200
;      TELEFAX:  512-474-7577
;      TELEX:  NOT APPLICABLE
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-908-317-33

  Query Match             100.0%;  Score 10;  DB 1;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
```

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                ||||||||||
Db          25 CTTCTCTTTT 34


RESULT 29
US-09-461-697-227/c
; Sequence 227, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 227
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-227

  Query Match             100.0%;  Score 10;  DB 3;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 30
PCT-US93-06171-33
; Sequence 33, Application PC/TUS9306171
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  FUSION PROTEINS COMPRISING
;    TITLE OF INVENTION:  EUKARYOTIC CYTOCHROME P450 FUSED TO
;    TITLE OF INVENTION:  A REDUCTASE
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06171
;      FILING DATE:  19930629
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/908,317
;      FILING DATE:  02 July 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PARKER, DAVID L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTSD:292/PAR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512-320-7200
;      TELEFAX:  512-474-7577
;      TELEX:  NOT APPLICABLE
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-06171-33

  Query Match             100.0%;  Score 10;  DB 5;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 34


RESULT 31
5258302-15/c
;Patent No. 5258302
;    APPLICANT: VEDVICK, THOMAS S.;ENGEL, MICHAEL E.;URCAN,
;MARY S.;BUCKHOLZ, RICHARD G.;KINNEY, JENNIFER A.
;    TITLE OF INVENTION: DNA FOR EXPRESSION OF APROTININ IN
;METHYLOTROPHIC YEAST CELLS
;    NUMBER OF SEQUENCES: 31
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/560,618
;      FILING DATE: 30-JUL-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 547,985
;      FILING DATE: 03-JUL-1990
;SEQ ID NO:15:
;      LENGTH: 43
5258302-15

  Query Match             100.0%;  Score 10;  DB 6;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 32
US-09-671-317-765
; Sequence 765, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Cohen, Annick
;  TITLE OF INVENTION:  BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
;  FILE REFERENCE:  62.US3.CIP
;  CURRENT APPLICATION NUMBER: US/09/671,317
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER:  US 09/536,178
;  PRIOR FILING DATE:  2000-03-23
;  PRIOR APPLICATION NUMBER:  PCT/IB00/00403
;  PRIOR FILING DATE:  2000-03-24
;  PRIOR APPLICATION NUMBER:  US 60/126,269
;  PRIOR FILING DATE:  1999-03-25
;  PRIOR APPLICATION NUMBER:  US 60/131,961
;  PRIOR FILING DATE:  1999-04-30
;  NUMBER OF SEQ ID NOS:  977
;  SOFTWARE:  Patent.pm
; SEQ ID NO 765
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
```

; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 12-602-196 : polymorphic base C or T
US-09-671-317-765

  Query Match 100.0%; Score 10; DB 4; Length 47;
  Best Local Similarity 100.0%; Pred. No. 1.9e+03;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
    ||||||||||
Db 1 CTTCTCTTTT 10

RESULT 33
US-09-422-978-522/c
; Sequence 522, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 522
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-15101-154 : polymorphic base G or C
US-09-422-978-522

  Query Match 100.0%; Score 10; DB 4; Length 47;
  Best Local Similarity 100.0%; Pred. No. 1.9e+03;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
    ||||||||||
Db 15 CTTCTCTTTT 6

RESULT 34
US-09-422-978-1282
; Sequence 1282, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1282
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-22604-208 : polymorphic base G or T
US-09-422-978-1282

  Query Match 100.0%; Score 10; DB 4; Length 47;
  Best Local Similarity 100.0%; Pred. No. 1.9e+03;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
    ||||||||||
Db 13 CTTCTCTTTT 22

RESULT 35
US-09-422-978-1546
; Sequence 1546, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1546
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-4541-39 : polymorphic base G or T
US-09-422-978-1546

  Query Match 100.0%; Score 10; DB 4; Length 47;
  Best Local Similarity 100.0%; Pred. No. 1.9e+03;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCTTTT 10
    ||||||||||
Db 9 CTTCTCTTTT 18

RESULT 36
US-09-422-978-2472/c
; Sequence 2472, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614

```
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2472
;    LENGTH: 47
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
;    FEATURE:
;    NAME/KEY: allele
;    LOCATION: 24
;    OTHER INFORMATION: 99-11191-86 : polymorphic base A or G
US-09-422-978-2472

  Query Match             100.0%;  Score 10;  DB 4;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         45 CTTCTCTTTT 36


RESULT 37
US-09-422-978-3284/c
; Sequence 3284, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3284
;    LENGTH: 47
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
;    FEATURE:
;    NAME/KEY: allele
;    LOCATION: 24
;    OTHER INFORMATION: 99-2981-53 : polymorphic base T or C
US-09-422-978-3284

  Query Match             100.0%;  Score 10;  DB 4;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         41 CTTCTCTTTT 32


RESULT 38
US-09-461-697-225/c
; Sequence 225, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 225
;    LENGTH: 48
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-461-697-225

  Query Match             100.0%;  Score 10;  DB 3;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 39
US-08-477-928A-37/c
; Sequence 37, Application US/08477928A
; Patent No. 6207389
;  GENERAL INFORMATION:
;    APPLICANT:  Dosch, Hans M.
;    TITLE OF INVENTION:  METHODS FOR CONTROLLING T
;    TITLE OF INVENTION:  LYMPHOCYTE MEDIATED IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BAKER & BOTTS
;      STREET:  1299 Pennsylvania Avenue
;      CITY:  Washington D.C.
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  20004-2400
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,928A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Remenick, James
;      REGISTRATION NUMBER:  36902
;      REFERENCE/DOCKET NUMBER:  19060-0105
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 639 7700
;      TELEFAX:  (202) 639 7890
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-477-928A-37

  Query Match             100.0%;  Score 10;  DB 3;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         42 CTTCTCTTTT 33


RESULT 40
US-08-910-632-40/c
```

```
; Sequence 40, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
;  APPLICANT: KOOL, ERIC T.
;  TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
;  FILE REFERENCE: 220.00010130
;  CURRENT APPLICATION NUMBER: US/08/910,632B
;  CURRENT FILING DATE: 1997-08-13
;  EARLIER APPLICATION NUMBER: 08/805,631
;  EARLIER FILING DATE: 1997-02-26
;  EARLIER APPLICATION NUMBER: 08/393,439
;  EARLIER FILING DATE: 1995-02-23
;  EARLIER APPLICATION NUMBER: 08/047,860
;  EARLIER FILING DATE: 1993-04-15
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
;   LENGTH: 53
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA 53mer circle
US-08-910-632-40

  Query Match             100.0%;  Score 10;  DB 3;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 41
US-08-910-632-41
; Sequence 41, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
;  APPLICANT: KOOL, ERIC T.
;  TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
;  FILE REFERENCE: 220.00010130
;  CURRENT APPLICATION NUMBER: US/08/910,632B
;  CURRENT FILING DATE: 1997-08-13
;  EARLIER APPLICATION NUMBER: 08/805,631
;  EARLIER FILING DATE: 1997-02-26
;  EARLIER APPLICATION NUMBER: 08/393,439
;  EARLIER FILING DATE: 1995-02-23
;  EARLIER APPLICATION NUMBER: 08/047,860
;  EARLIER FILING DATE: 1993-04-15
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 53
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: stem-loop RNA multimer which binds HIV-1 gag RNA
US-08-910-632-41

  Query Match             100.0%;  Score 10;  DB 3;  Length 53;
  Best Local Similarity    30.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              |::|:|::::
Db         38 CUUCUCUUUU 47


RESULT 42
US-08-805-631A-40/c
; Sequence 40, Application US/08805631A
; Patent No. 6096880
;  GENERAL INFORMATION:
;    APPLICANT:  UNIVERSITY OF ROCHESTER
;    TITLE OF INVENTION:  CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
;    TITLE OF INVENTION:  DNA
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MUETING, RAASCH & GEBHARDT, P.A.
;      STREET:  119 No. 6096880th Fourth Street, Suite 201
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,631A
;      FILING DATE:  26-FEB-97
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/393,439
;      FILING DATE:  23-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/047,860
;      FILING DATE:  15-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SANDBERG, VICTORIA A.
;      REGISTRATION NUMBER:  41,287
;      REFERENCE/DOCKET NUMBER:  220.00010140
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1226
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
US-08-805-631A-40

  Query Match             100.0%;  Score 10;  DB 3;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 43
US-08-805-631A-41
; Sequence 41, Application US/08805631A
; Patent No. 6096880
;  GENERAL INFORMATION:
;    APPLICANT:  UNIVERSITY OF ROCHESTER
;    TITLE OF INVENTION:  CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
;    TITLE OF INVENTION:  DNA
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MUETING, RAASCH & GEBHARDT, P.A.
;      STREET:  119 No. 6096880th Fourth Street, Suite 201
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/805,631A
;      FILING DATE:  26-FEB-97
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/393,439
;      FILING DATE:  23-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/047,860
;      FILING DATE:  15-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SANDBERG, VICTORIA A.
;      REGISTRATION NUMBER:  41,287
;      REFERENCE/DOCKET NUMBER:  220.00010140
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-305-1226
;      TELEFAX:  612-305-1228
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA (genomic)
US-08-805-631A-41

  Query Match             100.0%;  Score 10;  DB 3;  Length 53;
  Best Local Similarity   30.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              |::|:|::::
Db         38 CUUCUCUUUU 47


RESULT 44
US-09-569-344-40/c
; Sequence 40, Application US/09569344
; Patent No. 6368802
;   GENERAL INFORMATION:
;        APPLICANT: UNIVERSITY OF ROCHESTER
;        TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
;                            DNA
;        NUMBER OF SEQUENCES: 72
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 No. 6368802th Fourth Street, Suite 201
;             CITY: Minneapolis
;             STATE: Minnesota
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/569,344
;             FILING DATE: 11-May-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/805,631
;             FILING DATE: 26-FEB-97
;             APPLICATION NUMBER: US 08/393,439
;             FILING DATE: 23-FEB-1995
;             APPLICATION NUMBER: US 08/047,860
;             FILING DATE: 15-APR-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SANDBERG, VICTORIA A.
;             REGISTRATION NUMBER: 41,287
;             REFERENCE/DOCKET NUMBER: 220.00010140
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1226
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 53 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-569-344-40

  Query Match             100.0%;  Score 10;  DB 4;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 45
US-09-569-344-41
; Sequence 41, Application US/09569344
; Patent No. 6368802
;   GENERAL INFORMATION:
;        APPLICANT: UNIVERSITY OF ROCHESTER
;        TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
;                            DNA
;        NUMBER OF SEQUENCES: 72
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
;             STREET: 119 No. 6368802th Fourth Street, Suite 201
;             CITY: Minneapolis
;             STATE: Minnesota
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/569,344
;             FILING DATE: 11-May-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/805,631
;             FILING DATE: 26-FEB-97
;             APPLICATION NUMBER: US 08/393,439
;             FILING DATE: 23-FEB-1995
;             APPLICATION NUMBER: US 08/047,860
;             FILING DATE: 15-APR-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SANDBERG, VICTORIA A.
;             REGISTRATION NUMBER: 41,287
;             REFERENCE/DOCKET NUMBER: 220.00010140
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612-305-1226
;             TELEFAX: 612-305-1228
;   INFORMATION FOR SEQ ID NO: 41:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 53 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: RNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-569-344-41

  Query Match             100.0%;  Score 10;  DB 4;  Length 53;
  Best Local Similarity   30.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
```

```
                |::|:|::::
Db         38 CUUCUCUUUU 47


RESULT 46
US-08-585-684B-2533/c
; Sequence 2533, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2533:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  54 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-2533

  Query Match             100.0%;  Score 10;  DB 2;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 47
US-08-585-684B-2710/c
; Sequence 2710, Application US/08585684B
; Patent No. 5877021
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/585,684B
;      FILING DATE:  January 16, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/000,951
;      FILING DATE:  July 7, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2710:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  54 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-585-684B-2710

  Query Match             100.0%;  Score 10;  DB 2;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 48
US-09-038-073-2533/c
; Sequence 2533, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
```

```
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2533:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  54 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-2533

  Query Match             100.0%;  Score 10;  DB 3;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 49
US-09-038-073-2710/c
; Sequence 2710, Application US/09038073
; Patent No. 6194150
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Daniel T.
;    APPLICANT:  Jarvis, Thale
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  INDUCTION OF GRAFT TOLERANCE
;    TITLE OF INVENTION:  AND REVERSAL OF IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  2751
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,073
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/585,684
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2710:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  54 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-038-073-2710

  Query Match             100.0%;  Score 10;  DB 3;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 50
US-09-446-047A-1
; Sequence 1, Application US/09446047A
; Patent No. 6379924
;  GENERAL INFORMATION:
;       APPLICANT: Darrell Sleep
;                  Delta Biotechnology Limited
;       TITLE OF INVENTION: Improved Protein Expression Strains
;       NUMBER OF SEQUENCES: 20
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Aventis Behring LLC
;            STREET: 1020 First Avenue
;            CITY: King of Prussia
;            STATE: Pennsylvania
;            COUNTRY: United States of America
;            ZIP: 19406-1310
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/446,047A
;            FILING DATE: 15-Dec-1999
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 70 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "PCR primer"
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-446-047A-1

  Query Match             100.0%;  Score 10;  DB 4;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         30 CTTCTCTTTT 39


RESULT 51
US-08-117-374-5
; Sequence 5, Application US/08117374
; Patent No. 5362865
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5362865-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5362865th
;      CITY:  St. Louis
;      STATE:  Missouri
```

```
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/117,374
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-117-374-5

  Query Match             100.0%;  Score 10;  DB 1;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 52
US-08-280-263-5
; Sequence 5, Application US/08280263
; Patent No. 5659122
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5659122-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5659122th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/280,263
;      FILING DATE:  25-JUL-1994
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/117,374
;      FILING DATE:  02-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-280-263-5

  Query Match             100.0%;  Score 10;  DB 1;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 53
US-08-597-325-5
; Sequence 5, Application US/08597325
; Patent No. 6018100
;  GENERAL INFORMATION:
;    APPLICANT:  Rogers, Stephen G.
;    TITLE OF INVENTION:  Promoter for Transgenic Plants
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 6018100th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:  08/597,325
;      APPLICATION NUMBER:  US/08/597,325
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/366,240
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10647)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-597-325-5

  Query Match             100.0%;  Score 10;  DB 3;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 54
US-08-597-325-5
; Sequence 5, Application US/08597325
; Patent No. 6018100
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Rogers, Stephen G.
;    TITLE OF INVENTION:  Promoter for Transgenic Plants
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 6018100th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:  08/597,325
;      APPLICATION NUMBER:  US/08/597,325
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/366,240
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10647)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-597-325-5

  Query Match             100.0%;  Score 10;  DB 3;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 55
PCT-US94-10256-5
; Sequence 5, Application PC/TUS9410256
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  Non-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10256
;      FILING DATE:  01-SEPT-1994
;      CLASSIFICATION:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US94-10256-5

  Query Match             100.0%;  Score 10;  DB 5;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 56
US-08-117-374-6/c
; Sequence 6, Application US/08117374
; Patent No. 5362865
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5362865-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5362865th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/117,374
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  75 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-117-374-6

  Query Match             100.0%;  Score 10;  DB 1;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         33 CTTCTCTTTT 24


RESULT 57
US-08-280-263-6/c
; Sequence 6, Application US/08280263
; Patent No. 5659122
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5659122-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5659122th
;      CITY:  St. Louis
;      STATE:  Missouri
```

```
;       COUNTRY:  USA
;       ZIP:  63198
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/280,263
;       FILING DATE:  25-JUL-1994
;       CLASSIFICATION:  800
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/117,374
;       FILING DATE:  02-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Strode, Janelle D.
;       REGISTRATION NUMBER:  34,738
;       REFERENCE/DOCKET NUMBER:  38-21(10531)A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (314)537-6224
;       TELEFAX:  (314)537-6047
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  75 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-280-263-6

  Query Match             100.0%;  Score 10;  DB 1;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         33 CTTCTCTTTT 24


RESULT 58
US-08-597-325-6/c
; Sequence 6, Application US/08597325
; Patent No. 6018100
;  GENERAL INFORMATION:
;    APPLICANT:  Rogers, Stephen G.
;    TITLE OF INVENTION:  Promoter for Transgenic Plants
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 6018100th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:  08/597,325
;      APPLICATION NUMBER:  US/08/597,325
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/366,240
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10647)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  75 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-597-325-6

  Query Match             100.0%;  Score 10;  DB 3;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         33 CTTCTCTTTT 24


RESULT 59
US-08-597-325-6/c
; Sequence 6, Application US/08597325
; Patent No. 6018100
;  GENERAL INFORMATION:
;    APPLICANT:  Rogers, Stephen G.
;    TITLE OF INVENTION:  Promoter for Transgenic Plants
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 6018100th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:  08/597,325
;      APPLICATION NUMBER:  US/08/597,325
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/366,240
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10647)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  75 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-597-325-6

  Query Match             100.0%;  Score 10;  DB 3;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         33 CTTCTCTTTT 24


RESULT 60
PCT-US94-10256-6/c
; Sequence 6, Application PC/TUS9410256
```

```
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  Non-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10256
;      FILING DATE:  01-SEPT-1994
;      CLASSIFICATION:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  75 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US94-10256-6

  Query Match             100.0%;  Score 10;  DB 5;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         33 CTTCTCTTTT 24


RESULT 61
US-08-117-374-19
; Sequence 19, Application US/08117374
; Patent No. 5362865
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5362865-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5362865th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/117,374
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  78 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-117-374-19

  Query Match             100.0%;  Score 10;  DB 1;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 62
US-08-280-263-19
; Sequence 19, Application US/08280263
; Patent No. 5659122
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5659122-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5659122th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/280,263
;      FILING DATE:  25-JUL-1994
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/117,374
;      FILING DATE:  02-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  78 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-280-263-19

  Query Match             100.0%;  Score 10;  DB 1;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 63
PCT-US94-10256-19
; Sequence 19, Application PC/TUS9410256
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  Non-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10256
;      FILING DATE:  01-SEPT-1994
;      CLASSIFICATION:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  78 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US94-10256-19

  Query Match             100.0%;  Score 10;  DB 5;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 64
US-08-117-374-20/c
; Sequence 20, Application US/08117374
; Patent No. 5362865
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5362865-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5362865th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/117,374
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-117-374-20

  Query Match             100.0%;  Score 10;  DB 1;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         40 CTTCTCTTTT 31


RESULT 65
US-08-280-263-20/c
; Sequence 20, Application US/08280263
; Patent No. 5659122
;  GENERAL INFORMATION:
;    APPLICANT:  Austin, Glenn D.
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  No. 5659122-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle D. Strode, Monsanto Company, BB4F
;      STREET:  700 Chesterfield Parkway No. 5659122th
;      CITY:  St. Louis
;      STATE:  Missouri
;      COUNTRY:  USA
;      ZIP:  63198
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/280,263
;      FILING DATE:  25-JUL-1994
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/117,374
;      FILING DATE:  02-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Strode, Janelle D.
;      REGISTRATION NUMBER:  34,738
;      REFERENCE/DOCKET NUMBER:  38-21(10531)A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)537-6224
;      TELEFAX:  (314)537-6047
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-280-263-20

  Query Match             100.0%;  Score 10;  DB 1;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         40 CTTCTCTTTT 31


RESULT 66
PCT-US94-10256-20/c
; Sequence 20, Application PC/TUS9410256
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Enhanced Expression in Plants Using
;    TITLE OF INVENTION:  Non-translated Leader Sequences
;    NUMBER OF SEQUENCES:  22
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10256
;      FILING DATE:  01-SEPT-1994
;      CLASSIFICATION:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  82 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US94-10256-20

  Query Match             100.0%;  Score 10;  DB 5;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         40 CTTCTCTTTT 31


RESULT 67
US-09-174-465D-11/c
; Sequence 11, Application US/09174465D
; Patent No. 6180364
; GENERAL INFORMATION:
;  APPLICANT:  KOMAN, Ahment
;  APPLICANT:  CHASSIN, Dorine
;  APPLICANT:  BELLET, Dominique
;  TITLE OF INVENTION:  NEW PROTEIN CALLED EPIL/PLACENTIN, PROCESS FOR THE
;  TITLE OF INVENTION:  PREPARATION OF THIS PROTEIN AND PHARMACEUTICAL
;  TITLE OF INVENTION:  COMPOSITION CONTAINING SUCH, DNA CODING FOR SAID
;  TITLE OF INVENTION:  PROTEIN
;  FILE REFERENCE:  017753-103
;  CURRENT APPLICATION NUMBER: US/09/174,465D
;  CURRENT FILING DATE:  1998-10-19
;  PRIOR APPLICATION NUMBER:  US 08/482,842
;  PRIOR FILING DATE:  1995-06-07
;  NUMBER OF SEQ ID NOS:  16
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 93
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(93)
;   OTHER INFORMATION: Description of Unknown Organism:EPIL - Early
;   OTHER INFORMATION: Placenta Insulin-Like peptide
US-09-174-465D-11

  Query Match             100.0%;  Score 10;  DB 3;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 68
US-09-599-564A-11/c
; Sequence 11, Application US/09599564A
; Patent No. 6362318
; GENERAL INFORMATION:
;  APPLICANT: KOMAN, Ahment
;  APPLICANT:  CHASSIN, Dorine
;  APPLICANT:  BELLET, Dominique
;  TITLE OF INVENTION: NEW PROTEIN CALLED EPIL/PLACENTIN, PROCESS FOR THE
;  TITLE OF INVENTION:  PREPARATION OF THIS PROTEIN AND PHARMACEUTICAL
;  TITLE OF INVENTION:  COMPOSITION CONTAINING SUCH, DNA CODING FOR SAID
;  TITLE OF INVENTION:  PROTEIN
;  FILE REFERENCE: 017753-127
;  CURRENT APPLICATION NUMBER: US/09/599,564A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: 09/174,465
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: US 08/482,842
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 93
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(93)
;   OTHER INFORMATION: Description of Unknown Organism:EPIL - Early
;   OTHER INFORMATION: Placenta Insulin-Like peptide
US-09-599-564A-11

  Query Match             100.0%;  Score 10;  DB 4;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 69
US-09-461-697-223/c
; Sequence 223, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 223
;   LENGTH: 96
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-223

  Query Match             100.0%;  Score 10;  DB 3;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         68 CTTCTCTTTT 59


RESULT 70
US-09-144-428-55/c
; Sequence 55, Application US/09144428
; Patent No. 6583108
;  GENERAL INFORMATION:
;    APPLICANT:  BAYER CORPORATION, The
;    APPLICANT:  TAMBURINI, Paul P
;    APPLICANT:  DAVIS, Gary
;    APPLICANT:  DELARIA, Katherine A
;    APPLICANT:  MARLOR, Christopher W
;    APPLICANT:  MULLER, Daniel K
;    TITLE OF INVENTION:  HUMAN BIKUNIN
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
```

```
;       STREET:  300 S. Wacker Drive Suite 3200
;       CITY:  CHICAGO
;       STATE:  ILLINOIS
;       COUNTRY:  USA
;       ZIP:  60606
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/144,428
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US97/03894
;       FILING DATE:  10-MAR-1997
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/013,106
;       FILING DATE:  11-MAR-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/019,793
;       FILING DATE:  14-JUN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/725,251
;       FILING DATE:  04-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CHAO, Mark
;       REGISTRATION NUMBER:  37,293
;       REFERENCE/DOCKET NUMBER:  96,223-II
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 913-0001
;       TELEFAX:  (312) 913-0002
;   INFORMATION FOR SEQ ID NO:  55:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  102 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
US-09-144-428-55

  Query Match             100.0%;  Score 10;  DB 4;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         28 CTTCTCTTTT 19


RESULT 71
US-08-932-082-10
; Sequence 10, Application US/08932082
; Patent No. 6251856
;  GENERAL INFORMATION:
;    APPLICANT:  Markussen, Jan
;    APPLICANT:  Jonassen, Ib
;    APPLICANT:  Havelund, Svend
;    APPLICANT:  Brandt, Jakob
;    APPLICANT:  Kurtzhals, Peter
;    APPLICANT:  Hansen, Hertz Per
;    APPLICANT:  Kaarsholm, Niels Christian
;    TITLE OF INVENTION:  INSULIN DERIVATIVES
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6251856o No. 6251856disk of No. 6251856th America, Inc.
;      STREET:  405 Lexington Avenue, 64th Floor
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/932,082
;      FILING DATE:  12-AUG-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4341.204-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-867-0123
;      TELEFAX:  212-878-9655
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-932-082-10

  Query Match             100.0%;  Score 10;  DB 3;  Length 112;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         88 CTTCTCTTTT 97


RESULT 72
US-09-461-697-221/c
; Sequence 221, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 221
;   LENGTH: 117
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-221

  Query Match             100.0%;  Score 10;  DB 3;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         89 CTTCTCTTTT 80


RESULT 73
US-09-461-697-219/c
; Sequence 219, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
```

```
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 219
;   LENGTH: 126
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-219

  Query Match             100.0%;  Score 10;  DB 3;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         98 CTTCTCTTTT 89


RESULT 74
US-09-441-416A-22/c
; Sequence 22, Application US/09441416A
; Patent No. 6294518
; GENERAL INFORMATION:
;  APPLICANT: Potter, David A.
;  APPLICANT:  Skolnik, Paul R.
;  TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF
;  TITLE OF INVENTION:  CALPAIN
;  FILE REFERENCE: 00398-140001
;  CURRENT APPLICATION NUMBER: US/09/441,416A
;  CURRENT FILING DATE:  1999-11-16
;  PRIOR APPLICATION NUMBER: US 08/964,302
;  PRIOR FILING DATE: 1997-11-04
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 132
;   TYPE: DNA
;   ORGANISM: Eukaryote
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)...(129)
US-09-441-416A-22

  Query Match             100.0%;  Score 10;  DB 3;  Length 132;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         79 CTTCTCTTTT 70


RESULT 75
US-08-477-928A-36/c
; Sequence 36, Application US/08477928A
; Patent No. 6207389
;  GENERAL INFORMATION:
;    APPLICANT:  Dosch, Hans M.
;    TITLE OF INVENTION:  METHODS FOR CONTROLLING T
;    TITLE OF INVENTION:  LYMPHOCYTE MEDIATED IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BAKER & BOTTS
;      STREET:  1299 Pennsylvania Avenue
;      CITY:  Washington D.C.
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  20004-2400
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,928A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Remenick, James
;      REGISTRATION NUMBER:  36902
;      REFERENCE/DOCKET NUMBER:  19060-0105
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 639 7700
;      TELEFAX:  (202) 639 7890
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-477-928A-36

  Query Match             100.0%;  Score 10;  DB 3;  Length 146;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        138 CTTCTCTTTT 129


RESULT 76
US-09-461-697-217/c
; Sequence 217, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 217
;   LENGTH: 156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-217

  Query Match             100.0%;  Score 10;  DB 3;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
```

```
Db        128 CTTCTCTTTT 119


RESULT 77
US-09-461-697-215/c
; Sequence 215, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
;   LENGTH: 174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-215

  Query Match             100.0%;  Score 10;  DB 3;  Length 174;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        146 CTTCTCTTTT 137


RESULT 78
US-09-461-697-213/c
; Sequence 213, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 213
;   LENGTH: 189
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-213

  Query Match             100.0%;  Score 10;  DB 3;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        161 CTTCTCTTTT 152


RESULT 79
US-09-461-697-211/c
; Sequence 211, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 211
;   LENGTH: 195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-211

  Query Match             100.0%;  Score 10;  DB 3;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        167 CTTCTCTTTT 158


RESULT 80
US-09-107-532A-2918/c
; Sequence 2918, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 2918:
;        SEQUENCE CHARACTERISTICS:
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;            LENGTH: 198 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;        FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...198
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2918:
US-09-107-532A-2918

  Query Match            100.0%;  Score 10;  DB 4;  Length 198;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        126 CTTCTCTTTT 117


RESULT 81
US-09-107-532A-439
; Sequence 439, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 439:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 201 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;        FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...201
;        SEQUENCE DESCRIPTION: SEQ ID NO: 439:
US-09-107-532A-439

  Query Match            100.0%;  Score 10;  DB 4;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        177 CTTCTCTTTT 186


RESULT 82
US-09-107-532A-3253/c
; Sequence 3253, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3253:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 201 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;        FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...201
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3253:
US-09-107-532A-3253

  Query Match            100.0%;  Score 10;  DB 4;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        178 CTTCTCTTTT 169
```

```
RESULT 83
US-09-313-294A-7004
; Sequence 7004, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
;  APPLICANT:  Lalgudi, Raghunath V.
;  APPLICANT:  Ito, Laura Y.
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
;  FILE REFERENCE:  PL-0017 US
;  CURRENT APPLICATION NUMBER: US/09/313,294A
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS:  7600
;  SOFTWARE:  PERL Program
; SEQ ID NO 7004
;   LENGTH: 206
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6476212 700380982H1
;   NAME/KEY: unsure
;   LOCATION: 190, 193
;   OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7004

  Query Match             100.0%;  Score 10;  DB 4;  Length 206;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        129 CTTCTCTTTT 138


RESULT 84
US-09-461-697-209/c
; Sequence 209, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 209
;   LENGTH: 213
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-209

  Query Match             100.0%;  Score 10;  DB 3;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        185 CTTCTCTTTT 176


RESULT 85
5217891-19/c
;Patent No. 5217891
;    APPLICANT: BRAKE, ANTHONY J.;VAN DEN BERG, JOHAN A.
;    TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES
;A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS
;POLYPEPTIDES
;    NUMBER OF SEQUENCES: 23
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/507,398
;      FILING DATE: 09-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 78,551
;      FILING DATE: 28-JUL-1987
;SEQ ID NO:19:
;      LENGTH: 222
5217891-19

  Query Match             100.0%;  Score 10;  DB 6;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         37 CTTCTCTTTT 28


RESULT 86
US-09-016-434-99/c
; Sequence 99, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  99:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGFET03
;      CLONE:  1251228
US-09-016-434-99
```

```
  Query Match             100.0%;  Score 10;  DB 4;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         58 CTTCTCTTTT 49


RESULT 87
US-09-461-697-207/c
; Sequence 207, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT: Lo, Donald C.
;  APPLICANT: Barney, Shawn
;  APPLICANT: Thomas, Mary Beth
;  APPLICANT: Portbury, Stuart D.
;  APPLICANT: Puranam, Kasturi
;  APPLICANT: Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION: CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/461,697
;  CURRENT FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-461-697-207

  Query Match             100.0%;  Score 10;  DB 3;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        203 CTTCTCTTTT 194


RESULT 88
US-09-107-532A-2834/c
; Sequence 2834, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 2834:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 231 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...231
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2834:
US-09-107-532A-2834

  Query Match             100.0%;  Score 10;  DB 4;  Length 231;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         79 CTTCTCTTTT 70


RESULT 89
US-09-107-532A-724/c
; Sequence 724, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 724:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 234 base pairs
```

```
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...234
;        SEQUENCE DESCRIPTION: SEQ ID NO: 724:
US-09-107-532A-724

  Query Match            100.0%;  Score 10;  DB 4;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        118 CTTCTCTTTT 109


RESULT 90
US-09-397-787-56
; Sequence 56, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: King, Gordon E.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
;  TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
;  FILE REFERENCE: 210121.466C2
;  CURRENT APPLICATION NUMBER: US/09/397,787
;  CURRENT FILING DATE: 1999-09-16
;  NUMBER OF SEQ ID NOS: 334
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-397-787-56

  Query Match            100.0%;  Score 10;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         71 CTTCTCTTTT 80


RESULT 91
US-09-389-681-360
; Sequence 360, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
;  APPLICANT: Yuqui, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C3
;  CURRENT APPLICATION NUMBER: US/09/389,681A
;  CURRENT FILING DATE: 1999-09-02
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 360
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(241)
;   OTHER INFORMATION: n = A,T,C or G
US-09-389-681-360

  Query Match            100.0%;  Score 10;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        113 CTTCTCTTTT 122


RESULT 92
US-09-620-405B-360
; Sequence 360, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C8
;  CURRENT APPLICATION NUMBER: US/09/620,405B
;  CURRENT FILING DATE:  2000-07-20
;  NUMBER OF SEQ ID NOS: 495
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 360
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(241)
;   OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-360

  Query Match            100.0%;  Score 10;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        113 CTTCTCTTTT 122


RESULT 93
US-09-433-826B-360
; Sequence 360, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION:  COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.470C4
;  CURRENT APPLICATION NUMBER: US/09/433,826B
;  CURRENT FILING DATE:  1999-11-03
;  NUMBER OF SEQ ID NOS:  474
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 360
;   LENGTH: 241
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(241)
;   OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-360

  Query Match             100.0%;  Score 10;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db        113 CTTCTCTTTT 122


RESULT 94
US-09-604-287A-360
; Sequence 360, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Hepler, William T.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.470C7
;  CURRENT APPLICATION NUMBER: US/09/604,287A
;  CURRENT FILING DATE:  2000-06-22
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 360
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(241)
;   OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-360

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
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Db        113 CTTCTCTTTT 122


RESULT 95
US-09-016-434-737/c
; Sequence 737, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  737:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  TMLR2DT01
;      CLONE:  395476
US-09-016-434-737

  Query Match             100.0%;  Score 10;  DB 4;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
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Db        118 CTTCTCTTTT 109


RESULT 96
US-09-098-789-9
; Sequence 9, Application US/09098789
; Patent No. 6180342
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Tang, Y. Tom
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Patterson, Chandra
;    TITLE OF INVENTION:  VACULAR PROTON ATPASE SUBUNITS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/098,789
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CERRONE, MICHAEL C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0547 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
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;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  251 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  HIPONON02
;      CLONE:  2246348CT1
US-09-098-789-9

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Db        108 CTTCTCTTTT 117


RESULT 97
US-09-702-705-1077/c
; Sequence 1077, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C14
;  CURRENT APPLICATION NUMBER: US/09/702,705
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  1833
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1077
;   LENGTH: 256
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-702-705-1077

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        132 CTTCTCTTTT 123


RESULT 98
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; Sequence 1077, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1077
;   LENGTH: 256
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-1077

  Query Match             100.0%;  Score 10;  DB 4;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
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Db        132 CTTCTCTTTT 123


RESULT 99
US-09-313-294A-3143/c
; Sequence 3143, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
;  APPLICANT:  Lalgudi, Raghunath V.
;  APPLICANT:  Ito, Laura Y.
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
;  FILE REFERENCE:  PL-0017 US
;  CURRENT APPLICATION NUMBER: US/09/313,294A
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS:  7600
;  SOFTWARE:  PERL Program
; SEQ ID NO 3143
;   LENGTH: 263
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6476212 700610958H1
;   NAME/KEY: unsure
;   LOCATION: 216, 246
;   OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3143

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
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Db        166 CTTCTCTTTT 157


RESULT 100
US-09-134-001C-18/c
; Sequence 18, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 18
;   LENGTH: 267
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;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-18

  Query Match           100.0%;  Score 10;  DB 4;  Length 267;
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Qy          1 CTTCTCTTTT 10
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Db        159 CTTCTCTTTT 150


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Perfect score: 10
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Searched: 1792395 seqs, 1340900451 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	4	10	100.0	17	10	US-09-827-998-290	Sequence 290, App
c	5	10	100.0	17	10	US-09-827-998-291	Sequence 291, App
c	6	10	100.0	17	10	US-09-827-998-292	Sequence 292, App
c	7	10	100.0	17	10	US-09-827-998-293	Sequence 293, App
c	8	10	100.0	17	10	US-09-827-998-294	Sequence 294, App
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c	14	10	100.0	17	14	US-10-060-756A-1721	Sequence 1721, Ap
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c	16	10	100.0	17	14	US-10-060-756A-1723	Sequence 1723, Ap
c	17	10	100.0	17	14	US-10-060-756A-1724	Sequence 1724, Ap
c	18	10	100.0	17	14	US-10-060-756A-1725	Sequence 1725, Ap
c	19	10	100.0	17	14	US-10-060-756A-1726	Sequence 1726, Ap
c	20	10	100.0	17	14	US-10-060-756A-1727	Sequence 1727, Ap
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	22	10	100.0	19	12	US-10-205-309-609	Sequence 609, App
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c	25	10	100.0	24	11	US-09-934-489A-46	Sequence 46, Appl
c	26	10	100.0	24	12	US-10-438-729-167	Sequence 167, App
c	27	10	100.0	25	10	US-09-827-998-1102	Sequence 1102, Ap
c	28	10	100.0	25	10	US-09-827-998-1103	Sequence 1103, Ap
c	29	10	100.0	25	10	US-09-827-998-1104	Sequence 1104, Ap
c	30	10	100.0	25	10	US-09-827-998-1105	Sequence 1105, Ap
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c	34	10	100.0	25	10	US-09-827-998-1109	Sequence 1109, Ap
c	35	10	100.0	25	10	US-09-827-998-1110	Sequence 1110, Ap
c	36	10	100.0	25	10	US-09-827-998-1111	Sequence 1111, Ap
c	37	10	100.0	25	10	US-09-827-998-1112	Sequence 1112, Ap
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c	39	10	100.0	25	10	US-09-827-998-1114	Sequence 1114, Ap
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c	43	10	100.0	25	14	US-10-060-756A-3717	Sequence 3717, Ap
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c	45	10	100.0	25	14	US-10-060-756A-3719	Sequence 3719, Ap
c	46	10	100.0	25	14	US-10-060-756A-3720	Sequence 3720, Ap
c	47	10	100.0	25	14	US-10-060-756A-3721	Sequence 3721, Ap
c	48	10	100.0	25	14	US-10-060-756A-3722	Sequence 3722, Ap
c	49	10	100.0	25	14	US-10-060-756A-3723	Sequence 3723, Ap
c	50	10	100.0	25	14	US-10-060-756A-3724	Sequence 3724, Ap
c	51	10	100.0	25	14	US-10-060-756A-3725	Sequence 3725, Ap
c	52	10	100.0	25	14	US-10-060-756A-3726	Sequence 3726, Ap
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c	54	10	100.0	25	14	US-10-060-756A-3728	Sequence 3728, Ap
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c	56	10	100.0	25	14	US-10-060-756A-3730	Sequence 3730, Ap
c	57	10	100.0	25	14	US-10-060-756A-3731	Sequence 3731, Ap
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	67	10	100.0	25	14	US-10-098-263B-114427	Sequence 114427,
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	83	10	100.0	53	11	US-09-997-931-41	Sequence 41, Appl
	84	10	100.0	59	14	US-10-085-906-282	Sequence 282, App
	85	10	100.0	60	12	US-09-908-975-18382	Sequence 18382, A
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	89	10	100.0	61	10	US-09-946-807-1332	Sequence 1332, Ap

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	93	10	100.0	65	12	US-09-908-975-27615 Sequence 27615, A
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	95	10	100.0	65	12	US-10-032-585-135 Sequence 135, App
	96	10	100.0	65	12	US-10-032-585-152 Sequence 152, App
	97	10	100.0	65	12	US-10-032-585-2790 Sequence 2790, Ap
	98	10	100.0	76	14	US-10-015-637-3 Sequence 3, Appli
	99	10	100.0	81	12	US-10-029-386-24504 Sequence 24504, A
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	107	10	100.0	98	10	US-09-969-373-1521 Sequence 1521, Ap
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	110	10	100.0	104	9	US-09-864-761-31858 Sequence 31858, A
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	115	10	100.0	114	9	US-09-864-761-28863 Sequence 28863, A
c	116	10	100.0	117	10	US-09-922-261-221 Sequence 221, App
	117	10	100.0	118	12	US-10-029-386-15118 Sequence 15118, A
c	118	10	100.0	118	14	US-10-007-280A-122 Sequence 122, App
c	119	10	100.0	119	9	US-09-770-696-694 Sequence 694, App
	120	10	100.0	119	10	US-09-878-574-12732 Sequence 12732, A
	121	10	100.0	121	11	US-09-818-875-197 Sequence 197, App
c	122	10	100.0	121	11	US-09-818-875-198 Sequence 198, App
	123	10	100.0	121	11	US-09-818-875-213 Sequence 213, App
c	124	10	100.0	121	11	US-09-818-875-214 Sequence 214, App
	125	10	100.0	121	11	US-09-818-875-317 Sequence 317, App
c	126	10	100.0	121	11	US-09-818-875-318 Sequence 318, App
	127	10	100.0	121	11	US-09-818-875-321 Sequence 321, App
c	128	10	100.0	121	11	US-09-818-875-322 Sequence 322, App
	129	10	100.0	123	11	US-09-764-891-6108 Sequence 6108, Ap
	130	10	100.0	123	11	US-09-764-891-6109 Sequence 6109, Ap
c	131	10	100.0	125	9	US-09-294-093B-56 Sequence 56, Appl
	132	10	100.0	125	9	US-09-563-817-780 Sequence 780, App
c	133	10	100.0	126	10	US-09-922-261-219 Sequence 219, App
c	134	10	100.0	126	12	US-10-029-386-19178 Sequence 19178, A
	135	10	100.0	129	9	US-09-864-761-29992 Sequence 29992, A
	136	10	100.0	132	9	US-09-864-761-22578 Sequence 22578, A
c	137	10	100.0	132	11	US-09-962-967A-22 Sequence 22, Appl
	138	10	100.0	134	12	US-10-029-386-15576 Sequence 15576, A
	139	10	100.0	135	12	US-10-029-386-27260 Sequence 27260, A
	140	10	100.0	138	13	US-10-040-739-1495 Sequence 1495, Ap
c	141	10	100.0	140	9	US-09-864-761-23358 Sequence 23358, A
	142	10	100.0	146	9	US-09-864-761-27845 Sequence 27845, A
c	143	10	100.0	148	12	US-10-029-386-14189 Sequence 14189, A
c	144	10	100.0	149	12	US-10-247-813-25 Sequence 25, Appl
	145	10	100.0	150	10	US-09-969-373-201 Sequence 201, App
	146	10	100.0	150	12	US-10-029-386-21722 Sequence 21722, A
c	147	10	100.0	154	10	US-09-933-797-615 Sequence 615, App
	148	10	100.0	155	12	US-10-029-386-21326 Sequence 21326, A
c	149	10	100.0	156	10	US-09-922-261-217 Sequence 217, App
c	150	10	100.0	156	10	US-09-974-300-4171 Sequence 4171, Ap
	151	10	100.0	157	11	US-09-754-853A-244 Sequence 244, App
	152	10	100.0	163	9	US-09-770-696-391 Sequence 391, App
c	153	10	100.0	163	14	US-10-060-036-2004 Sequence 2004, Ap
	154	10	100.0	169	9	US-09-777-564-695 Sequence 695, App
	155	10	100.0	169	10	US-09-560-863-675 Sequence 675, App
	156	10	100.0	169	14	US-10-015-219-695 Sequence 695, App
c	157	10	100.0	173	9	US-09-770-696-331 Sequence 331, App
c	158	10	100.0	174	9	US-09-864-761-29931 Sequence 29931, A
c	159	10	100.0	174	10	US-09-922-261-215 Sequence 215, App
c	160	10	100.0	175	12	US-09-814-353-6379 Sequence 6379, Ap
c	161	10	100.0	175	12	US-09-814-353-12656 Sequence 12656, A
c	162	10	100.0	175	12	US-10-029-386-21262 Sequence 21262, A
	163	10	100.0	178	10	US-09-764-847-327 Sequence 327, App
	164	10	100.0	178	14	US-10-092-154-327 Sequence 327, App
	165	10	100.0	181	11	US-09-754-853A-287 Sequence 287, App
	166	10	100.0	182	10	US-09-954-531-893 Sequence 893, App
	167	10	100.0	183	9	US-09-864-761-22682 Sequence 22682, A
c	168	10	100.0	184	10	US-09-765-231A-48 Sequence 48, Appl
c	169	10	100.0	186	9	US-09-864-761-31276 Sequence 31276, A
	170	10	100.0	186	12	US-09-802-668-5 Sequence 5, Appli
	171	10	100.0	186	12	US-10-243-475-5 Sequence 5, Appli
c	172	10	100.0	189	10	US-09-922-261-213 Sequence 213, App
	173	10	100.0	189	14	US-10-083-357-555 Sequence 555, App
	174	10	100.0	192	9	US-09-864-761-24940 Sequence 24940, A
	175	10	100.0	192	10	US-09-878-574-6130 Sequence 6130, Ap
c	176	10	100.0	194	13	US-10-001-879-67 Sequence 67, Appl
c	177	10	100.0	195	10	US-09-922-261-211 Sequence 211, App
c	178	10	100.0	198	10	US-09-765-231A-69 Sequence 69, Appl
	179	10	100.0	201	9	US-09-736-969A-80 Sequence 80, Appl
c	180	10	100.0	201	10	US-09-878-574-9594 Sequence 9594, Ap
c	181	10	100.0	201	10	US-09-974-300-4222 Sequence 4222, Ap
c	182	10	100.0	201	12	US-10-238-075-1160 Sequence 1160, Ap
c	183	10	100.0	201	12	US-10-029-386-17528 Sequence 17528, A
c	184	10	100.0	202	10	US-09-104-408-9 Sequence 9, Appli
	185	10	100.0	202	12	US-10-029-386-15138 Sequence 15138, A
	186	10	100.0	203	9	US-09-815-242-2754 Sequence 2754, Ap
	187	10	100.0	203	12	US-10-029-386-18965 Sequence 18965, A
	188	10	100.0	204	9	US-09-864-761-17394 Sequence 17394, A
	189	10	100.0	206	10	US-09-983-965-5827 Sequence 5827, Ap
	190	10	100.0	208	10	US-09-796-692-9479 Sequence 9479, Ap
	191	10	100.0	208	14	US-10-040-862-9479 Sequence 9479, Ap
	192	10	100.0	210	9	US-09-864-761-27524 Sequence 27524, A
c	193	10	100.0	210	14	US-10-001-254-1 Sequence 1, Appli
	194	10	100.0	212	12	US-10-055-728-70 Sequence 70, Appl
c	195	10	100.0	213	10	US-09-878-574-13095 Sequence 13095, A
c	196	10	100.0	213	10	US-09-922-261-209 Sequence 209, App
c	197	10	100.0	215	12	US-10-287-274-45 Sequence 45, Appl
	198	10	100.0	217	9	US-09-923-876-1193 Sequence 1193, Ap
c	199	10	100.0	218	9	US-09-864-761-18972 Sequence 18972, A
	200	10	100.0	218	10	US-09-867-701-10089 Sequence 10089, A
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	202	10	100.0	225	14	US-10-040-862-9189 Sequence 9189, Ap
c	203	10	100.0	226	9	US-09-563-817-279 Sequence 279, App
c	204	10	100.0	226	12	US-10-116-712-342 Sequence 342, App
c	205	10	100.0	228	10	US-09-974-300-5635 Sequence 5635, Ap
	206	10	100.0	229	8	US-08-781-986A-4596 Sequence 4596, Ap
	207	10	100.0	230	14	US-10-102-524-560 Sequence 560, App
	208	10	100.0	231	9	US-09-864-761-21191 Sequence 21191, A
c	209	10	100.0	231	10	US-09-922-261-207 Sequence 207, App
	210	10	100.0	231	10	US-09-796-692-3380 Sequence 3380, Ap
	211	10	100.0	231	14	US-10-040-862-3380 Sequence 3380, Ap
	212	10	100.0	232	14	US-10-060-036-1883 Sequence 1883, Ap
	213	10	100.0	233	9	US-09-864-761-29261 Sequence 29261, A
	214	10	100.0	238	12	US-10-029-386-25781 Sequence 25781, A
c	215	10	100.0	239	9	US-09-923-876-2173 Sequence 2173, Ap
c	216	10	100.0	239	13	US-10-040-739-23 Sequence 23, Appl
c	217	10	100.0	240	9	US-09-294-093B-1275 Sequence 1275, Ap
	218	10	100.0	241	9	US-09-604-287A-360 Sequence 360, App
	219	10	100.0	241	9	US-09-876-889-56 Sequence 56, Appl
	220	10	100.0	241	11	US-09-551-621-360 Sequence 360, App
	221	10	100.0	241	12	US-10-124-805-360 Sequence 360, App
	222	10	100.0	241	13	US-10-007-805-360 Sequence 360, App
	223	10	100.0	241	14	US-10-076-622-360 Sequence 360, App
c	224	10	100.0	242	10	US-09-969-373-1053 Sequence 1053, Ap
	225	10	100.0	250	9	US-09-294-093B-289 Sequence 289, App
c	226	10	100.0	250	9	US-09-294-093B-289 Sequence 289, App
c	227	10	100.0	253	10	US-09-880-107-2807 Sequence 2807, Ap
c	228	10	100.0	254	12	US-09-237-183A-2137 Sequence 2137, Ap
c	229	10	100.0	255	12	US-09-814-353-16251 Sequence 16251, A
c	230	10	100.0	256	10	US-09-736-457-1077 Sequence 1077, Ap
c	231	10	100.0	256	10	US-09-902-941-1077 Sequence 1077, Ap
c	232	10	100.0	256	10	US-09-849-626-1077 Sequence 1077, Ap
c	233	10	100.0	256	11	US-09-764-891-978 Sequence 978, App
c	234	10	100.0	256	12	US-10-113-872-1077 Sequence 1077, Ap
c	235	10	100.0	256	14	US-10-017-754-1077 Sequence 1077, Ap

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c 237	10	100.0	259	9	US-09-864-761-17354	Sequence 17354, A
c 238	10	100.0	259	11	US-09-910-009A-276	Sequence 276, App
c 239	10	100.0	259	11	US-09-910-009A-296	Sequence 296, App
c 240	10	100.0	260	10	US-09-878-574-6452	Sequence 6452, Ap
241	10	100.0	260	10	US-09-783-590-3894	Sequence 3894, Ap
c 242	10	100.0	261	9	US-09-923-876-691	Sequence 691, App
243	10	100.0	261	10	US-09-924-035A-802	Sequence 802, App
c 244	10	100.0	261	10	US-09-104-408-8	Sequence 8, Appli
c 245	10	100.0	262	11	US-09-910-009A-273	Sequence 273, App
c 246	10	100.0	263	10	US-09-878-574-10506	Sequence 10506, A
247	10	100.0	263	12	US-10-116-712-150	Sequence 150, App
c 248	10	100.0	264	10	US-09-878-574-13953	Sequence 13953, A
c 249	10	100.0	265	7	US-08-973-363-12	Sequence 12, Appl
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251	10	100.0	265	10	US-09-878-574-15398	Sequence 15398, A
c 252	10	100.0	265	10	US-09-764-864-753	Sequence 753, App
c 253	10	100.0	265	11	US-09-764-891-299	Sequence 299, App
c 254	10	100.0	266	10	US-09-878-574-9893	Sequence 9893, Ap
c 255	10	100.0	266	10	US-09-878-574-13464	Sequence 13464, A
256	10	100.0	266	10	US-09-920-300A-125	Sequence 125, App
257	10	100.0	266	12	US-10-099-926-125	Sequence 125, App
258	10	100.0	266	13	US-10-033-528-125	Sequence 125, App
259	10	100.0	267	9	US-09-815-242-919	Sequence 919, App
c 260	10	100.0	267	10	US-09-925-637-39	Sequence 39, Appl
261	10	100.0	267	10	US-09-878-574-14229	Sequence 14229, A
262	10	100.0	267	10	US-09-783-590-10635	Sequence 10635, A
263	10	100.0	267	13	US-10-027-632-68332	Sequence 68332, A
c 264	10	100.0	267	14	US-10-084-205-39	Sequence 39, Appl
c 265	10	100.0	268	9	US-09-294-093B-1042	Sequence 1042, Ap
c 266	10	100.0	268	9	US-09-294-093B-4784	Sequence 4784, Ap
c 267	10	100.0	268	10	US-09-960-352-11467	Sequence 11467, A
268	10	100.0	269	10	US-09-878-574-7022	Sequence 7022, Ap
c 269	10	100.0	270	9	US-09-815-242-8639	Sequence 8639, Ap
c 270	10	100.0	270	10	US-09-878-574-1759	Sequence 1759, Ap
271	10	100.0	270	10	US-09-878-574-14565	Sequence 14565, A
c 272	10	100.0	270	10	US-09-878-574-15479	Sequence 15479, A
c 273	10	100.0	271	9	US-09-294-093B-4373	Sequence 4373, Ap
274	10	100.0	271	9	US-09-923-876-804	Sequence 804, App
275	10	100.0	271	10	US-09-960-352-7929	Sequence 7929, Ap
c 276	10	100.0	272	9	US-09-923-876-756	Sequence 756, App
277	10	100.0	272	10	US-09-878-574-14990	Sequence 14990, A
278	10	100.0	273	10	US-09-878-574-6606	Sequence 6606, Ap
c 279	10	100.0	273	10	US-09-878-574-7347	Sequence 7347, Ap
c 280	10	100.0	273	10	US-09-974-300-4940	Sequence 4940, Ap
c 281	10	100.0	273	12	US-10-050-054-4	Sequence 4, Appli
282	10	100.0	274	10	US-09-878-574-13744	Sequence 13744, A
c 283	10	100.0	274	10	US-09-878-574-14893	Sequence 14893, A
c 284	10	100.0	274	10	US-09-796-692-4996	Sequence 4996, Ap
c 285	10	100.0	274	14	US-10-040-862-4996	Sequence 4996, Ap
c 286	10	100.0	276	10	US-09-878-574-12618	Sequence 12618, A
c 287	10	100.0	276	10	US-09-960-352-9746	Sequence 9746, Ap
c 288	10	100.0	277	10	US-09-878-574-9630	Sequence 9630, Ap
289	10	100.0	277	10	US-09-878-574-12185	Sequence 12185, A
290	10	100.0	278	9	US-09-294-093B-5812	Sequence 5812, Ap
c 291	10	100.0	279	10	US-09-878-574-10946	Sequence 10946, A
292	10	100.0	280	10	US-09-878-574-5464	Sequence 5464, Ap
293	10	100.0	280	10	US-09-878-574-9624	Sequence 9624, Ap
294	10	100.0	280	13	US-10-040-739-1275	Sequence 1275, Ap
295	10	100.0	280	13	US-10-114-893-82	Sequence 82, Appl
c 296	10	100.0	281	11	US-09-535-459-1982	Sequence 1982, Ap
297	10	100.0	282	10	US-09-878-574-14613	Sequence 14613, A
c 298	10	100.0	282	10	US-09-922-261-205	Sequence 205, App
299	10	100.0	283	10	US-09-878-574-8079	Sequence 8079, Ap
300	10	100.0	283	10	US-09-878-574-8106	Sequence 8106, Ap
301	10	100.0	284	10	US-09-728-444-868	Sequence 868, App
302	10	100.0	284	10	US-09-764-868-1394	Sequence 1394, Ap
303	10	100.0	285	10	US-09-878-574-5136	Sequence 5136, Ap
304	10	100.0	285	12	US-10-029-386-22548	Sequence 22548, A
c 305	10	100.0	286	10	US-09-104-408-7	Sequence 7, Appli
306	10	100.0	286	12	US-09-814-353-3363	Sequence 3363, Ap
307	10	100.0	286	12	US-09-814-353-9684	Sequence 9684, Ap
c 308	10	100.0	287	13	US-10-027-632-286859	Sequence 286859,
c 309	10	100.0	287	14	US-10-198-846-12391	Sequence 12391, A
310	10	100.0	288	10	US-09-924-035A-451	Sequence 451, App
c 311	10	100.0	289	13	US-10-027-632-132435	Sequence 132435,
312	10	100.0	290	9	US-09-923-876-3204	Sequence 3204, Ap
c 313	10	100.0	291	10	US-09-974-300-3908	Sequence 3908, Ap
314	10	100.0	291	10	US-09-728-444-86	Sequence 86, Appl
315	10	100.0	291	10	US-09-728-444-323	Sequence 323, App
c 316	10	100.0	291	10	US-09-796-692-409	Sequence 409, App
c 317	10	100.0	291	10	US-09-796-692-5551	Sequence 5551, Ap
318	10	100.0	291	10	US-09-796-692-5708	Sequence 5708, Ap
c 319	10	100.0	291	13	US-10-040-739-850	Sequence 850, App
c 320	10	100.0	291	14	US-10-040-862-409	Sequence 409, App
c 321	10	100.0	291	14	US-10-040-862-5551	Sequence 5551, Ap
322	10	100.0	291	14	US-10-040-862-5708	Sequence 5708, Ap
c 323	10	100.0	292	10	US-09-878-574-15342	Sequence 15342, A
324	10	100.0	293	10	US-09-867-701-982	Sequence 982, App
c 325	10	100.0	293	12	US-10-116-712-393	Sequence 393, App
326	10	100.0	293	13	US-10-040-739-982	Sequence 982, App
c 327	10	100.0	294	9	US-09-815-242-817	Sequence 817, App
c 328	10	100.0	294	10	US-09-938-842A-2410	Sequence 2410, Ap
c 329	10	100.0	295	13	US-10-027-632-51616	Sequence 51616, A
c 330	10	100.0	296	11	US-09-535-459-1989	Sequence 1989, Ap
c 331	10	100.0	298	9	US-09-294-093B-91	Sequence 91, Appl
332	10	100.0	300	9	US-09-294-093B-4274	Sequence 4274, Ap
333	10	100.0	300	10	US-09-878-574-14684	Sequence 14684, A
334	10	100.0	300	12	US-10-116-712-189	Sequence 189, App
c 335	10	100.0	301	10	US-09-783-590-1545	Sequence 1545, Ap
336	10	100.0	302	10	US-09-833-381-1023	Sequence 1023, Ap
c 337	10	100.0	303	10	US-09-867-701-9833	Sequence 9833, Ap
338	10	100.0	304	10	US-09-783-590-3831	Sequence 3831, Ap
c 339	10	100.0	304	10	US-09-796-692-5252	Sequence 5252, Ap
c 340	10	100.0	304	13	US-10-027-632-287973	Sequence 287973,
c 341	10	100.0	304	14	US-10-040-862-5252	Sequence 5252, Ap
c 342	10	100.0	305	9	US-09-294-093B-5643	Sequence 5643, Ap
c 343	10	100.0	306	10	US-09-922-261-203	Sequence 203, App
c 344	10	100.0	306	12	US-09-769-744A-9	Sequence 9, Appli
345	10	100.0	306	12	US-10-116-712-152	Sequence 152, App
c 346	10	100.0	307	14	US-10-102-524-1038	Sequence 1038, Ap
c 347	10	100.0	308	11	US-09-764-891-507	Sequence 507, App
c 348	10	100.0	309	9	US-09-764-878-235	Sequence 235, App
349	10	100.0	309	12	US-09-814-353-2425	Sequence 2425, Ap
350	10	100.0	309	12	US-09-814-353-8762	Sequence 8762, Ap
c 351	10	100.0	309	14	US-10-079-854-235	Sequence 235, App
c 352	10	100.0	309	14	US-10-060-036-2124	Sequence 2124, Ap
353	10	100.0	311	10	US-09-783-590-6308	Sequence 6308, Ap
c 354	10	100.0	311	10	US-09-880-107-1640	Sequence 1640, Ap
355	10	100.0	311	12	US-09-814-353-3216	Sequence 3216, Ap
356	10	100.0	311	12	US-09-814-353-9541	Sequence 9541, Ap
c 357	10	100.0	313	10	US-09-960-352-4597	Sequence 4597, Ap
c 358	10	100.0	313	10	US-09-880-107-54	Sequence 54, Appl
359	10	100.0	315	10	US-09-878-574-5243	Sequence 5243, Ap
360	10	100.0	316	10	US-09-880-107-1818	Sequence 1818, Ap
c 361	10	100.0	316	10	US-09-736-457-1553	Sequence 1553, Ap
c 362	10	100.0	316	10	US-09-902-941-1553	Sequence 1553, Ap
c 363	10	100.0	316	10	US-09-849-626-1553	Sequence 1553, Ap
c 364	10	100.0	316	11	US-09-803-719-1074	Sequence 1074, Ap
365	10	100.0	316	12	US-09-814-353-15255	Sequence 15255, A
c 366	10	100.0	316	12	US-10-113-872-1553	Sequence 1553, Ap
c 367	10	100.0	316	12	US-10-029-386-25509	Sequence 25509, A
c 368	10	100.0	316	14	US-10-017-754-1553	Sequence 1553, Ap
c 369	10	100.0	317	12	US-10-116-712-447	Sequence 447, App
370	10	100.0	318	11	US-09-803-719-1053	Sequence 1053, Ap
371	10	100.0	318	12	US-09-814-353-3893	Sequence 3893, Ap
372	10	100.0	318	12	US-09-814-353-10201	Sequence 10201, A
373	10	100.0	318	13	US-10-027-632-126233	Sequence 126233,
374	10	100.0	319	10	US-09-867-701-126	Sequence 126, App
c 375	10	100.0	319	12	US-09-942-052-724	Sequence 724, App
c 376	10	100.0	319	12	US-09-942-052-725	Sequence 725, App
c 377	10	100.0	319	12	US-09-942-052-726	Sequence 726, App
c 378	10	100.0	320	9	US-09-759-143-224	Sequence 224, App
c 379	10	100.0	320	9	US-09-780-669-224	Sequence 224, App
c 380	10	100.0	320	9	US-09-030-606-224	Sequence 224, App
c 381	10	100.0	320	9	US-09-822-827-224	Sequence 224, App

c 382	10	100.0	320	9	US-09-115-453-224	Sequence 224, App
383	10	100.0	320	10	US-09-878-574-3072	Sequence 3072, Ap
384	10	100.0	320	10	US-09-764-864-545	Sequence 545, App
c 385	10	100.0	320	10	US-09-232-880-224	Sequence 224, App
c 386	10	100.0	320	10	US-09-895-793-224	Sequence 224, App
c 387	10	100.0	320	10	US-09-895-814-224	Sequence 224, App
c 388	10	100.0	320	11	US-09-803-719-1955	Sequence 1955, Ap
c 389	10	100.0	320	12	US-10-144-678A-224	Sequence 224, App
390	10	100.0	320	12	US-09-814-353-4429	Sequence 4429, Ap
391	10	100.0	320	12	US-09-814-353-10732	Sequence 10732, A
c 392	10	100.0	320	12	US-10-294-025-224	Sequence 224, App
c 393	10	100.0	320	13	US-10-012-896-224	Sequence 224, App
c 394	10	100.0	320	14	US-10-010-940-224	Sequence 224, App
c 395	10	100.0	321	11	US-09-910-009A-151	Sequence 151, App
396	10	100.0	321	11	US-09-918-995-6771	Sequence 6771, Ap
c 397	10	100.0	322	11	US-09-535-459-1981	Sequence 1981, Ap
398	10	100.0	324	10	US-09-833-381-1209	Sequence 1209, Ap
c 399	10	100.0	324	14	US-10-169-048-45	Sequence 45, Appl
400	10	100.0	325	10	US-09-969-708-506	Sequence 506, App
401	10	100.0	325	10	US-09-954-456-1667	Sequence 1667, Ap
402	10	100.0	325	10	US-09-880-107-1838	Sequence 1838, Ap
c 403	10	100.0	326	8	US-08-781-986A-4309	Sequence 4309, Ap
c 404	10	100.0	326	11	US-09-910-009A-194	Sequence 194, App
405	10	100.0	326	12	US-09-814-353-664	Sequence 664, App
406	10	100.0	326	12	US-09-814-353-7040	Sequence 7040, Ap
c 407	10	100.0	327	10	US-09-764-847-1130	Sequence 1130, Ap
408	10	100.0	327	11	US-09-803-719-899	Sequence 899, App
409	10	100.0	327	11	US-09-764-891-2070	Sequence 2070, Ap
410	10	100.0	327	12	US-10-116-712-180	Sequence 180, App
c 411	10	100.0	327	14	US-10-092-154-1130	Sequence 1130, Ap
c 412	10	100.0	328	10	US-09-764-847-1129	Sequence 1129, Ap
c 413	10	100.0	328	14	US-10-092-154-1129	Sequence 1129, Ap
414	10	100.0	329	11	US-09-803-719-278	Sequence 278, App
415	10	100.0	330	10	US-09-867-701-8778	Sequence 8778, Ap
c 416	10	100.0	330	14	US-10-083-357-254	Sequence 254, App
c 417	10	100.0	331	13	US-10-027-632-285358	Sequence 285358,
c 418	10	100.0	332	12	US-10-029-386-24244	Sequence 24244, A
419	10	100.0	332	12	US-10-116-712-446	Sequence 446, App
c 420	10	100.0	332	12	US-10-116-712-470	Sequence 470, App
421	10	100.0	333	10	US-09-867-701-110	Sequence 110, App
422	10	100.0	333	12	US-09-814-353-4006	Sequence 4006, Ap
423	10	100.0	333	12	US-09-814-353-10314	Sequence 10314, A
424	10	100.0	333	12	US-09-814-353-19427	Sequence 19427, A
c 425	10	100.0	334	9	US-09-770-791-926	Sequence 926, App
c 426	10	100.0	334	10	US-09-783-590-1635	Sequence 1635, Ap
c 427	10	100.0	334	11	US-09-918-995-18886	Sequence 18886, A
c 428	10	100.0	335	9	US-09-784-423-26	Sequence 26, Appl
429	10	100.0	335	10	US-09-983-965-3102	Sequence 3102, Ap
c 430	10	100.0	335	10	US-09-796-692-6576	Sequence 6576, Ap
c 431	10	100.0	335	13	US-10-027-632-288453	Sequence 288453,
c 432	10	100.0	335	14	US-10-040-862-6576	Sequence 6576, Ap
c 433	10	100.0	336	10	US-09-974-300-8266	Sequence 8266, Ap
c 434	10	100.0	336	12	US-10-238-075-555	Sequence 555, App
c 435	10	100.0	337	10	US-09-929-493-7	Sequence 7, Appli
c 436	10	100.0	337	11	US-09-803-719-1668	Sequence 1668, Ap
c 437	10	100.0	337	11	US-09-918-995-17973	Sequence 17973, A
c 438	10	100.0	338	12	US-10-270-487-7	Sequence 7, Appli
c 439	10	100.0	339	11	US-09-803-719-963	Sequence 963, App
440	10	100.0	339	13	US-10-027-632-128730	Sequence 128730,
c 441	10	100.0	339	14	US-10-060-036-1565	Sequence 1565, Ap
442	10	100.0	339	14	US-10-313-542-168	Sequence 168, App
443	10	100.0	340	10	US-09-920-300A-423	Sequence 423, App
444	10	100.0	340	12	US-10-099-926-423	Sequence 423, App
445	10	100.0	340	13	US-10-033-528-423	Sequence 423, App
c 446	10	100.0	342	9	US-09-770-791-814	Sequence 814, App
c 447	10	100.0	342	11	US-09-918-995-18543	Sequence 18543, A
448	10	100.0	342	12	US-10-116-712-589	Sequence 589, App
c 449	10	100.0	343	11	US-09-803-719-1667	Sequence 1667, Ap
450	10	100.0	343	12	US-10-125-159-81	Sequence 81, Appl
451	10	100.0	344	12	US-10-116-712-134	Sequence 134, App
452	10	100.0	345	9	US-09-770-791-775	Sequence 775, App
453	10	100.0	346	10	US-09-969-708-371	Sequence 371, App
454	10	100.0	346	10	US-09-969-708-436	Sequence 436, App
455	10	100.0	346	12	US-09-873-319-233	Sequence 233, App
456	10	100.0	346	12	US-09-960-706-386	Sequence 386, App
457	10	100.0	346	14	US-10-228-794-81	Sequence 81, Appl
458	10	100.0	346	14	US-10-106-698-2735	Sequence 2735, Ap
459	10	100.0	347	10	US-09-867-701-10233	Sequence 10233, A
460	10	100.0	347	12	US-10-116-712-614	Sequence 614, App
c 461	10	100.0	347	14	US-10-060-036-1825	Sequence 1825, Ap
c 462	10	100.0	348	9	US-09-864-761-2092	Sequence 2092, Ap
c 463	10	100.0	348	10	US-09-867-701-2327	Sequence 2327, Ap
464	10	100.0	348	12	US-09-814-353-3169	Sequence 3169, Ap
465	10	100.0	348	12	US-09-814-353-9494	Sequence 9494, Ap
c 466	10	100.0	349	10	US-09-867-701-9513	Sequence 9513, Ap
c 467	10	100.0	349	10	US-09-974-300-3225	Sequence 3225, Ap
468	10	100.0	349	11	US-09-764-891-1286	Sequence 1286, Ap
c 469	10	100.0	349	13	US-10-040-739-889	Sequence 889, App
470	10	100.0	350	9	US-09-770-791-705	Sequence 705, App
471	10	100.0	350	13	US-10-027-632-54299	Sequence 54299, A
472	10	100.0	350	13	US-10-027-632-180119	Sequence 180119,
c 473	10	100.0	351	10	US-09-867-701-854	Sequence 854, App
474	10	100.0	353	10	US-09-560-863-669	Sequence 669, App
475	10	100.0	353	10	US-09-960-352-7434	Sequence 7434, Ap
476	10	100.0	353	10	US-09-983-965-155	Sequence 155, App
c 477	10	100.0	353	11	US-09-955-999-35	Sequence 35, Appl
478	10	100.0	353	11	US-09-803-719-945	Sequence 945, App
479	10	100.0	353	11	US-09-803-719-1506	Sequence 1506, Ap
c 480	10	100.0	354	9	US-09-815-242-9617	Sequence 9617, Ap
c 481	10	100.0	354	10	US-09-764-847-80	Sequence 80, Appl
c 482	10	100.0	354	10	US-09-938-842A-5319	Sequence 5319, Ap
c 483	10	100.0	354	14	US-10-092-154-80	Sequence 80, Appl
484	10	100.0	355	9	US-09-770-791-618	Sequence 618, App
c 485	10	100.0	355	10	US-09-867-701-2400	Sequence 2400, Ap
486	10	100.0	356	10	US-09-867-701-170	Sequence 170, App
487	10	100.0	356	10	US-09-867-701-2002	Sequence 2002, Ap
488	10	100.0	356	11	US-09-918-995-29782	Sequence 29782, A
489	10	100.0	356	11	US-09-764-891-1552	Sequence 1552, Ap
c 490	10	100.0	356	12	US-10-161-051-17	Sequence 17, Appl
c 491	10	100.0	357	9	US-09-764-887-148	Sequence 148, App
492	10	100.0	357	10	US-09-867-701-2408	Sequence 2408, Ap
c 493	10	100.0	357	14	US-10-073-961-148	Sequence 148, App
494	10	100.0	358	9	US-09-864-761-11220	Sequence 11220, A
495	10	100.0	358	11	US-09-918-995-7467	Sequence 7467, Ap
c 496	10	100.0	359	10	US-09-783-590-1751	Sequence 1751, Ap
c 497	10	100.0	359	12	US-09-814-353-21980	Sequence 21980, A
c 498	10	100.0	359	14	US-10-102-524-1534	Sequence 1534, Ap
c 499	10	100.0	360	9	US-09-777-564-810	Sequence 810, App
500	10	100.0	360	9	US-09-864-761-27334	Sequence 27334, A

ALIGNMENTS

```
RESULT 1
US-09-827-998-287/c
; Sequence 287, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 287
;    LENGTH: 17
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-827-998-287
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  Query Match           100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 2
US-09-827-998-288/c
; Sequence 288, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 288
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-288

  Query Match           100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 3
US-09-827-998-289/c
; Sequence 289, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 289
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-289

  Query Match           100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 4
US-09-827-998-290/c
; Sequence 290, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 290
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-290

  Query Match           100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 5
US-09-827-998-291/c
; Sequence 291, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 291
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-291

  Query Match           100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 6
US-09-827-998-292/c
; Sequence 292, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
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;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 292
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-292

  Query Match            100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 7
US-09-827-998-293/c
; Sequence 293, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 293
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-293

  Query Match            100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 8
US-09-827-998-294/c
; Sequence 294, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 294
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-294

  Query Match            100.0%;  Score 10;  DB 10;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 9
US-09-930-423-1740/c
; Sequence 1740, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: MBHB00,918-A 400/027
;  CURRENT APPLICATION NUMBER: US/09/930,423
;  CURRENT FILING DATE:  2001-08-15
;  NUMBER OF SEQ ID NOS: 4553
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1740
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-09-930-423-1740

  Query Match            100.0%;  Score 10;  DB 11;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 10
US-09-930-423-1741/c
; Sequence 1741, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: MBHB00,918-A 400/027
;  CURRENT APPLICATION NUMBER: US/09/930,423
;  CURRENT FILING DATE:  2001-08-15
;  NUMBER OF SEQ ID NOS: 4553
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1741
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-09-930-423-1741

  Query Match            100.0%;  Score 10;  DB 11;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3
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RESULT 11
US-09-745-237A-1740/c
; Sequence 1740, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: 400/007 (MBHB00-918-A)
;  CURRENT APPLICATION NUMBER: US/09/745,237A
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 4550
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1740
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-745-237A-1740

  Query Match             100.0%;  Score 10;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 12
US-09-745-237A-1741/c
; Sequence 1741, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: 400/007 (MBHB00-918-A)
;  CURRENT APPLICATION NUMBER: US/09/745,237A
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 4550
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1741
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-745-237A-1741

  Query Match             100.0%;  Score 10;  DB 12;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 13
US-10-060-756A-1720/c
; Sequence 1720, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1720
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1720

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 14
US-10-060-756A-1721/c
; Sequence 1721, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1721
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1721

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 15
US-10-060-756A-1722/c
```

```
; Sequence 1722, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1722
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1722

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 16
US-10-060-756A-1723/c
; Sequence 1723, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1723
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1723

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 17
US-10-060-756A-1724/c
; Sequence 1724, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1724
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1724

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 18
US-10-060-756A-1725/c
; Sequence 1725, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1725
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1725

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 19
US-10-060-756A-1726/c
; Sequence 1726, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian    ,
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1726
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1726

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 20
US-10-060-756A-1727/c
; Sequence 1727, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1727
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-1727

  Query Match             100.0%;  Score 10;  DB 14;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 21
US-10-205-309-284/c
; Sequence 284, Application US/10205309
; Publication No. US20030190635A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Usin
;  TITLE OF INVENTION:  Interfering RNA
;  FILE REFERENCE: 900/033
;  CURRENT APPLICATION NUMBER: US/10/205,309
;  CURRENT FILING DATE:  2002-10-25
;  NUMBER OF SEQ ID NOS: 674
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target sequence/siNA sense
US-10-205-309-284

  Query Match             100.0%;  Score 10;  DB 12;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 22
US-10-205-309-609
; Sequence 609, Application US/10205309
; Publication No. US20030190635A1
; GENERAL INFORMATION:
```

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;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
;  TITLE OF INVENTION:  Interfering RNA
;  FILE REFERENCE: 900/033
;  CURRENT APPLICATION NUMBER: US/10/205,309
;  CURRENT FILING DATE:  2002-10-25
;  NUMBER OF SEQ ID NOS: 674
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 609
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-205-309-609

  Query Match             100.0%;  Score 10;  DB 12;  Length 19;
  Best Local Similarity   30.0%;  Pred. No. 1.6e+04;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              |::|:|::::
Db         10 CUUCUCUUUU 19


RESULT 23
US-10-087-325-15/c
; Sequence 15, Application US/10087325
; Publication No. US20020192682A1
; GENERAL INFORMATION:
;  APPLICANT: Escary, Jean-Louis
;  TITLE OF INVENTION: NEW POLYNUCLEOTIDES AND POLYPEPTIDES OF THE IFNalpha-2 GENE
;  FILE REFERENCE: 021349/0010
;  CURRENT APPLICATION NUMBER: US/10/087,325
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: FR 0102843
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-087-325-15

  Query Match             100.0%;  Score 10;  DB 13;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 24
US-09-853-830-168/c
; Sequence 168, Application US/09853830
; Patent No. US20020107388A1
; GENERAL INFORMATION:
;  APPLICANT: Vandenbark, Arthur A.
;  TITLE OF INVENTION: Methods of Identifying and Monitoring
;  TITLE OF INVENTION:  Disease-Associated T Cells
;  FILE REFERENCE: P-IM 4734
;  CURRENT APPLICATION NUMBER: US/09/853,830
;  CURRENT FILING DATE:  2001-09-18
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-853-830-168

  Query Match             100.0%;  Score 10;  DB 10;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 25
US-09-934-489A-46/c
; Sequence 46, Application US/09934489A
; Publication No. US20030108872A1
; GENERAL INFORMATION:
;  APPLICANT: Sulavik, Mark
;  APPLICANT:  Ling, Losee Lucy
;  APPLICANT:  Opperman, Tim
;  APPLICANT:  Moir, Don
;  APPLICANT:  Bunker, Christopher
;  TITLE OF INVENTION: Genomics-Assisted Rapid Identification of Targets
;  FILE REFERENCE: 032796-082
;  CURRENT APPLICATION NUMBER: US/09/934,489A
;  CURRENT FILING DATE:  2001-08-23
;  PRIOR APPLICATION NUMBER: US 60/226,896
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-09-934-489A-46

  Query Match             100.0%;  Score 10;  DB 11;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 26
US-10-438-729-167/c
; Sequence 167, Application US/10438729
; Publication No. US20030190665A1
; GENERAL INFORMATION:
;  APPLICANT: Vandenbark, Arthur
;  TITLE OF INVENTION: METHODS OF SELECTING T CELL RECEPTOR V PEPTIDES FOR THERAPEUTIC
;  FILE REFERENCE: 6915-65828
;  CURRENT APPLICATION NUMBER: US/10/438,729
;  CURRENT FILING DATE:  2003-05-14
;  PRIOR APPLICATION NUMBER: 60/203,984
;  PRIOR FILING DATE: 2000-05-12
;  PRIOR APPLICATION NUMBER: 09/853,830
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 60/380,731
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-438-729-167

  Query Match             100.0%;  Score 10;  DB 12;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
```

```
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 27
US-09-827-998-1102/c
; Sequence 1102, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1102
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1102

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 28
US-09-827-998-1103/c
; Sequence 1103, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1103
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1103

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         24 CTTCTCTTTT 15


RESULT 29
US-09-827-998-1104/c
; Sequence 1104, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1104
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1104

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 30
US-09-827-998-1105/c
; Sequence 1105, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1105
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1105

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 31
US-09-827-998-1106/c
; Sequence 1106, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
```

```
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1106
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1106

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 32
US-09-827-998-1107/c
; Sequence 1107, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1107
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1107

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 33
US-09-827-998-1108/c
; Sequence 1108, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1108
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1108

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 34
US-09-827-998-1109/c
; Sequence 1109, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1109
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1109

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 35
US-09-827-998-1110/c
; Sequence 1110, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1110
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1110

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
```

```
Db         17 CTTCTCTTTT 8


RESULT 36
US-09-827-998-1111/c
; Sequence 1111, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1111
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1111

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 37
US-09-827-998-1112/c
; Sequence 1112, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1112
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1112

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 38
US-09-827-998-1113/c
; Sequence 1113, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1113
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1113

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 39
US-09-827-998-1114/c
; Sequence 1114, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1114
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1114

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 40
US-09-827-998-1115/c
; Sequence 1115, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
```

```
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1115
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1115

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 41
US-09-827-998-1116/c
; Sequence 1116, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1116
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1116

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 42
US-09-827-998-1117/c
; Sequence 1117, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
;  APPLICANT: Gu, Yizhong
;  APPLICANT:  Shannon, Mark
;  TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
;  FILE REFERENCE: MDhMORF-8
;  CURRENT APPLICATION NUMBER: US/09/827,998
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1881
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1117
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-827-998-1117

  Query Match             100.0%;  Score 10;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 43
US-10-060-756A-3717/c
; Sequence 3717, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3717
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3717

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 44
US-10-060-756A-3718/c
; Sequence 3718, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
```

```
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3718
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3718

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         24 CTTCTCTTTT 15


RESULT 45
US-10-060-756A-3719/c
; Sequence 3719, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3719
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3719

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 46
US-10-060-756A-3720/c
; Sequence 3720, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3720
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3720

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         22 CTTCTCTTTT 13


RESULT 47
US-10-060-756A-3721/c
; Sequence 3721, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3721
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3721

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
```

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              ||||||||||
Db         21 CTTCTCTTTT 12


RESULT 48
US-10-060-756A-3722/c
; Sequence 3722, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3722
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3722

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 49
US-10-060-756A-3723/c
; Sequence 3723, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3723
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3723

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         19 CTTCTCTTTT 10


RESULT 50
US-10-060-756A-3724/c
; Sequence 3724, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3724
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3724

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         18 CTTCTCTTTT 9


RESULT 51
US-10-060-756A-3725/c
; Sequence 3725, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
```

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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3725
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3725

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 8


RESULT 52
US-10-060-756A-3726/c
; Sequence 3726, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3726
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3726

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 7


RESULT 53
US-10-060-756A-3727/c
; Sequence 3727, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3727
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3727

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 6


RESULT 54
US-10-060-756A-3728/c
; Sequence 3728, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3728
;   LENGTH: 25
```

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3728

  Query Match            100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 55
US-10-060-756A-3729/c
; Sequence 3729, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3729
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3729

  Query Match            100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 56
US-10-060-756A-3730/c
; Sequence 3730, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3730
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3730

  Query Match            100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 57
US-10-060-756A-3731/c
; Sequence 3731, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3731
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3731

  Query Match            100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 2


RESULT 58
US-10-060-756A-3732/c
; Sequence 3732, Application US/10060756A
; Publication No. US20030046717A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Jian
;  TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
;  FILE REFERENCE: PB0177
;  CURRENT APPLICATION NUMBER: US/10/060,756A
;  CURRENT FILING DATE:  2002-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 09/864,761
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/327,898
;  PRIOR FILING DATE: 2001-10-09
;  NUMBER OF SEQ ID NOS: 4804
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 3732
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-756A-3732

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         10 CTTCTCTTTT 1


RESULT 59
US-10-215-112-7249/c
; Sequence 7249, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  TITLE OF INVENTION: Method of Genetic Analysis of Probes:
;  TITLE OF INVENTION:  Test3
;  FILE REFERENCE: 3119
;  CURRENT APPLICATION NUMBER: US/10/215,112
;  CURRENT FILING DATE:  2002-08-08
;  NUMBER OF SEQ ID NOS: 14936
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7249
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7249

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 60
US-10-215-112-7250/c
; Sequence 7250, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  TITLE OF INVENTION: Method of Genetic Analysis of Probes:
;  TITLE OF INVENTION:  Test3
;  FILE REFERENCE: 3119
;  CURRENT APPLICATION NUMBER: US/10/215,112
;  CURRENT FILING DATE:  2002-08-08
;  NUMBER OF SEQ ID NOS: 14936
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7250
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7250

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 61
US-10-215-112-7372/c
; Sequence 7372, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  TITLE OF INVENTION: Method of Genetic Analysis of Probes:
;  TITLE OF INVENTION:  Test3
;  FILE REFERENCE: 3119
;  CURRENT APPLICATION NUMBER: US/10/215,112
;  CURRENT FILING DATE:  2002-08-08
;  NUMBER OF SEQ ID NOS: 14936
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7372
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7372

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 3


RESULT 62
US-10-098-263B-6553
; Sequence 6553, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 6553
;   LENGTH: 25
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapien
US-10-098-263B-6553

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          7 CTTCTCTTTT 16


RESULT 63
US-10-098-263B-10333
; Sequence 10333, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 10333
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-10333

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          5 CTTCTCTTTT 14


RESULT 64
US-10-098-263B-34049
; Sequence 34049, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 34049
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-34049

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         11 CTTCTCTTTT 20


RESULT 65
US-10-098-263B-41737/c
; Sequence 41737, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41737
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-41737

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 4


RESULT 66
US-10-098-263B-86720/c
; Sequence 86720, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86720
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-86720

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 67
US-10-098-263B-114427
; Sequence 114427, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114427
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
```

US-10-098-263B-114427

Query Match 100.0%; Score 10; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 25
```

RESULT 68
US-10-098-263B-114428
; Sequence 114428, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114428
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-114428

Query Match 100.0%; Score 10; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 25
```

RESULT 69
US-10-098-263B-118057
; Sequence 118057, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118057
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118057

Query Match 100.0%; Score 10; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 24
```

RESULT 70
US-10-098-263B-118058
; Sequence 118058, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118058
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118058

Query Match 100.0%; Score 10; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 24
```

RESULT 71
US-10-098-263B-118243
; Sequence 118243, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118243
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118243

Query Match 100.0%; Score 10; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 24
```

RESULT 72
US-10-098-263B-118244
; Sequence 118244, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118244
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118244

```
  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 24


RESULT 73
US-10-098-263B-119613
; Sequence 119613, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 119613
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-119613

  Query Match             100.0%;  Score 10;  DB 14;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         13 CTTCTCTTTT 22


RESULT 74
US-09-765-272-359/c
; Sequence 359, Application US/09765272
; Patent No. US20020061545A1
;   GENERAL INFORMATION:
;        APPLICANT: Choi et. al.
;        TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
;        NUMBER OF SEQUENCES: 452
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/765,272
;             FILING DATE: 22-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/961,083
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brookes, A. Anders
;             REGISTRATION NUMBER: 36,373
;             REFERENCE/DOCKET NUMBER: PB340P2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (301) 309-8504
;             TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 359:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 33 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 359:
US-09-765-272-359

  Query Match             100.0%;  Score 10;  DB 9;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         23 CTTCTCTTTT 14


RESULT 75
US-09-780-533A-2783/c
; Sequence 2783, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2783
;   LENGTH: 38
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-533A-2783

  Query Match             100.0%;  Score 10;  DB 11;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 29


RESULT 76
US-09-780-533A-4693
; Sequence 4693, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Chowrira, Bharat
;  APPLICANT:  Haeberli, Pete
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;  FILE REFERENCE: MBHB00,878-A (400/011)
;  CURRENT APPLICATION NUMBER: US/09/780,533A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,797
;  PRIOR FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 6679
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4693
;   LENGTH: 38
```

```
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-780-533A-4693

  Query Match            100.0%;  Score 10;  DB 11;  Length 38;
  Best Local Similarity   30.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              |::|:|::::
Db         29 CUUCUCUUUU 38


RESULT 77
US-09-877-478-4478
; Sequence 4478, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Draper, Kenneth
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Morrissey, Dave
;  TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;  FILE REFERENCE: MBHB00-845-H (400/029)
;  CURRENT APPLICATION NUMBER: US/09/877,478
;  CURRENT FILING DATE:  2001-12-31
;  PRIOR APPLICATION NUMBER: US 07/882,712
;  PRIOR FILING DATE: 1992-05-14
;  PRIOR APPLICATION NUMBER: US 09/531,025
;  PRIOR FILING DATE: 2000-03-20
;  PRIOR APPLICATION NUMBER: US 09/636,385
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: US 09/696,347
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 08/193,627
;  PRIOR FILING DATE: 1994-02-07
;  PRIOR APPLICATION NUMBER: US 08/433,993
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 08/434,504
;  PRIOR FILING DATE: 1995-05-04
;  PRIOR APPLICATION NUMBER: US 09/436,430
;  PRIOR FILING DATE: 1999-11-08
;  NUMBER OF SEQ ID NOS: 6586
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4478
;   LENGTH: 38
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
;   NAME/KEY: misc_feature
;   LOCATION: (11)..(16)
;   OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
;   NAME/KEY: misc_feature
;   LOCATION: (20)..(20)
;   OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
;   NAME/KEY: misc_feature
;   LOCATION: (22)..(22)
;   OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
;   NAME/KEY: misc_feature
;   LOCATION: (24)..(25)
;   OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
;   NAME/KEY: misc_feature
;   LOCATION: (30)..(30)
;   OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
US-09-877-478-4478

  Query Match            100.0%;  Score 10;  DB 11;  Length 38;
  Best Local Similarity   30.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              |::|:|::::
Db         29 CUUCUCUUUU 38


RESULT 78
US-09-792-818-944/c
; Sequence 944, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Jarvis, Thale
;  APPLICANT:  Von Carlowitz, Ira
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Hamblin, Paul
;  APPLICANT:  Ellis, Jonathan
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
;  TITLE OF INVENTION:  (GRID) Gene
;  FILE REFERENCE: MBHB00-901-A (400/013)
;  CURRENT APPLICATION NUMBER: US/09/792,818
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS: 2304
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 944
;   LENGTH: 38
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-09-792-818-944

  Query Match            100.0%;  Score 10;  DB 12;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         38 CTTCTCTTTT 29


RESULT 79
US-09-922-261-227/c
; Sequence 227, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT:  Lo, Donald C.
;  APPLICANT:  Barney, Shawn
;  APPLICANT:  Thomas, Mary Beth
;  APPLICANT:  Portbury, Stuart D.
;  APPLICANT:  Puranam, Kasturi
;  APPLICANT:  Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION:  CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/922,261
;  CURRENT FILING DATE:  2001-08-03
;  PRIOR APPLICATION NUMBER: US/09/461,697
;  PRIOR FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 227
;   LENGTH: 42
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-922-261-227

  Query Match            100.0%;  Score 10;  DB 10;  Length 42;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         14 CTTCTCTTTT 5


RESULT 80
US-10-032-585-1923
; Sequence 1923, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1923
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-1923

  Query Match             100.0%;  Score 10;  DB 12;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         12 CTTCTCTTTT 21


RESULT 81
US-09-922-261-225/c
; Sequence 225, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
;  APPLICANT: COGENT NEUROSCIENCE, Inc.
;  APPLICANT:  Lo, Donald C.
;  APPLICANT:  Barney, Shawn
;  APPLICANT:  Thomas, Mary Beth
;  APPLICANT:  Portbury, Stuart D.
;  APPLICANT:  Puranam, Kasturi
;  APPLICANT:  Katz, Lawrence C.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
;  TITLE OF INVENTION:  CELL DEATH
;  FILE REFERENCE: 10001-005-999
;  CURRENT APPLICATION NUMBER: US/09/922,261
;  CURRENT FILING DATE:  2001-08-03
;  PRIOR APPLICATION NUMBER: US/09/461,697
;  PRIOR FILING DATE: 1999-12-14
;  NUMBER OF SEQ ID NOS: 466
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 225
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-922-261-225

  Query Match             100.0%;  Score 10;  DB 10;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         20 CTTCTCTTTT 11


RESULT 82
US-09-997-931-40/c
; Sequence 40, Application US/09997931
; Publication No. US20030087241A1
; GENERAL INFORMATION:
;  APPLICANT: University of Rochester
;  APPLICANT:  Kool, Eric
;  TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
;  FILE REFERENCE: 220.00010142
;  CURRENT APPLICATION NUMBER: US/09/997,931
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: US 09/569,344
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 08/805,631
;  PRIOR FILING DATE: 1997-02-26
;  PRIOR APPLICATION NUMBER: US 08/393,439
;  PRIOR FILING DATE: 1995-02-23
;  PRIOR APPLICATION NUMBER: US 08/047,860
;  PRIOR FILING DATE: 1993-04-15
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 53
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 53mer circle
US-09-997-931-40

  Query Match             100.0%;  Score 10;  DB 11;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 16


RESULT 83
US-09-997-931-41
; Sequence 41, Application US/09997931
; Publication No. US20030087241A1
; GENERAL INFORMATION:
;  APPLICANT: University of Rochester
;  APPLICANT:  Kool, Eric
;  TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
;  FILE REFERENCE: 220.00010142
;  CURRENT APPLICATION NUMBER: US/09/997,931
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: US 09/569,344
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 08/805,631
;  PRIOR FILING DATE: 1997-02-26
;  PRIOR APPLICATION NUMBER: US 08/393,439
;  PRIOR FILING DATE: 1995-02-23
;  PRIOR APPLICATION NUMBER: US 08/047,860
;  PRIOR FILING DATE: 1993-04-15
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
;   LENGTH: 53
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: stem-loop multimer which binds HIV-1 gag RNA
US-09-997-931-41

  Query Match             100.0%;  Score 10;  DB 11;  Length 53;
  Best Local Similarity    30.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CTTCTCTTTT 10
              |::|:|::::
Db         38 CUUCUCUUUU 47
```

RESULT 84
US-10-085-906-282
; Sequence 282, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-282

Query Match 100.0%; Score 10; DB 14; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         45 CTTCTCTTTT 54
```

RESULT 85
US-09-908-975-18382
; Sequence 18382, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18382
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18382

Query Match 100.0%; Score 10; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52
```

RESULT 86
US-09-908-975-31961/c
; Sequence 31961, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31961
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-31961

Query Match 100.0%; Score 10; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         48 CTTCTCTTTT 39
```

RESULT 87
US-09-795-668-1332
; Sequence 1332, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1332
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1332

Query Match 100.0%; Score 10; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26
```

RESULT 88
US-09-795-686-1332

```
; Sequence 1332, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2005-001
;  CURRENT APPLICATION NUMBER: US/09/795,686
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,715
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1332
;   LENGTH: 61
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-686-1332

  Query Match             100.0%;  Score 10;  DB 9;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26


RESULT 89
US-09-946-807-1332
; Sequence 1332, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/946,807
;  CURRENT FILING DATE:  2001-09-05
;  PRIOR APPLICATION NUMBER: US/09/795,668
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1332
;   LENGTH: 61
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-946-807-1332

  Query Match             100.0%;  Score 10;  DB 10;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         17 CTTCTCTTTT 26


RESULT 90
US-10-027-632-58348
; Sequence 58348, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58348
;   LENGTH: 61
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-58348

  Query Match             100.0%;  Score 10;  DB 13;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         16 CTTCTCTTTT 25


RESULT 91
US-09-983-965-5096
; Sequence 5096, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 37-21(10297)C
;  CURRENT APPLICATION NUMBER: US/09/983,965
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: US 09/465,231
;  PRIOR FILING DATE: 1999-12-15
;  PRIOR APPLICATION NUMBER: US 60/113,678
;  PRIOR FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5096
;   LENGTH: 63
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 31-LIB34-084-Q1-E1-H11
US-09-983-965-5096

  Query Match             100.0%;  Score 10;  DB 10;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         24 CTTCTCTTTT 33


RESULT 92
US-10-085-906-276/c
; Sequence 276, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
;  APPLICANT: Ying, Vincent
;  APPLICANT:  Wu, Paul
```

```
;  APPLICANT:  Gray, Gary S.
;  TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
;  TITLE OF INVENTION:  COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
;  FILE REFERENCE: GNN-5343CP2
;  CURRENT APPLICATION NUMBER: US/10/085,906
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 60/126,215
;  PRIOR FILING DATE: 1999-03-25
;  PRIOR APPLICATION NUMBER: US 09/534,061
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: PCT/US00/07938
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 545
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 276
;   LENGTH: 64
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-085-906-276

  Query Match            100.0%;  Score 10;  DB 14;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 34


RESULT 93
US-09-908-975-27615
; Sequence 27615, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0005
;  CURRENT APPLICATION NUMBER: US/09/908,975
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/287,724
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/221,607
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 32337
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27615
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-908-975-27615

  Query Match            100.0%;  Score 10;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         47 CTTCTCTTTT 56


RESULT 94
US-09-908-975-28061/c
; Sequence 28061, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
;  APPLICANT: SHOSHAN, Avi
;  APPLICANT:  WASSERMAN, Alon
;  APPLICANT:  MINTZ, Eli
;  APPLICANT:  MINTZ, Liat
;  APPLICANT:  FAIGLER, Simchon
;  TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
;  TITLE OF INVENTION:  THAT POPULATE A TRANSCRIPTOME
;  FILE REFERENCE: 36688-0005
;  CURRENT APPLICATION NUMBER: US/09/908,975
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/287,724
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/221,607
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 32337
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28061
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-908-975-28061

  Query Match            100.0%;  Score 10;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         41 CTTCTCTTTT 32


RESULT 95
US-10-032-585-135
; Sequence 135, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-135

  Query Match            100.0%;  Score 10;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db          2 CTTCTCTTTT 11


RESULT 96
US-10-032-585-152
; Sequence 152, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 152
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-152

  Query Match             100.0%;  Score 10;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         15 CTTCTCTTTT 24


RESULT 97
US-10-032-585-2790
; Sequence 2790, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
;  APPLICANT: Terry, Roemer D.
;  APPLICANT:  Bo, Jiang
;  APPLICANT:  Charles, Boone
;  APPLICANT:  Howard, Bussey
;  TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;  FILE REFERENCE: 10182-005-999
;  CURRENT APPLICATION NUMBER: US/10/032,585
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 8000
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2790
;   LENGTH: 65
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-10-032-585-2790

  Query Match             100.0%;  Score 10;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         25 CTTCTCTTTT 34


RESULT 98
US-10-015-637-3
; Sequence 3, Application US/10015637
; Publication No. US20030046727A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Qi
;  APPLICANT:  Dubois, Patrice
;  APPLICANT:  Liang, Jihong
;  APPLICANT:  Oulmassov, Tim
;  TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof
;  FILE REFERENCE: 13587.106
;  CURRENT APPLICATION NUMBER: US/10/015,637
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: US 60/255879
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 76
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-015-637-3

  Query Match             100.0%;  Score 10;  DB 14;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
              ||||||||||
Db         43 CTTCTCTTTT 52


RESULT 99
US-10-029-386-24504
; Sequence 24504, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24504
;   LENGTH: 81
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR18.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;   OTHER INFORMATION: EST_HUMAN HIT: AW905636.1, EVALUE 9.00e-02
US-10-029-386-24504

  Query Match             100.0%;  Score 10;  DB 12;  Length 81;
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Qy          1 CTTCTCTTTT 10
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Db         29 CTTCTCTTTT 38


RESULT 100
US-10-029-386-17114/c
; Sequence 17114, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17114
;   LENGTH: 84
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL137017.4
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;   OTHER INFORMATION: EST_HUMAN HIT: BE536158.1, EVALUE 9.50e-02
;   OTHER INFORMATION: NT HIT: X03248.1, EVALUE 1.00e+00
US-10-029-386-17114

  Query Match             100.0%;  Score 10;  DB 12;  Length 84;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTCTCTTTT 10
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Db 18 CTTCTCTTTT 9

Search completed: October 28, 2003, 18:49:54
Job time : 1754 secs